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FIGURE 1

CGCCCGCGCGCGGGCTCAACTTTGTAGAGCGAGGGGCCAACTTGGCAGAGCGCGCGGCCA
GCTTTGCAGAGAGCGCCCTCCAGGGACTATGCGTGCGGGGACACGGGATCTACCCATACC
ATTGACTAACTATGGAAGATTATACCAAAATAGAGAAAATTGGAGAAGGTACCTATGGAG
TTGTGTATAAGGGTAGACACAAAACCTACAGGTCAAGTGGTAGCCATGAAAAAATCAGAC
TAGAAAGTGAAGAGGAAGGGGTTCCTAGTACTGCAATTCGGGAAATTTCTCTATTAAAGG
AACTTCGTCATCCAAATATAGTCAGTCTTCAGGATGTGCTTATGCAGGATTCCAGGTTAT
ATCTCATCTTTGAGTTTCTTTCCATGGATCTGAAGAAATACTTGGATTCTATCCCTCCTG
GTCAGTACATGGATTCTTCACTTGTTAAGGTAGTAACACTCTGGTACAGATCTCCAGAAG
TATTGCTGGGGTCAGCTCGTTACTCAACTCCAGTTGACATTTGGAGTATAGGCACCATAT
TTGCTGAAGTAGCAACTAAGAAACCACTTTTCCATGGGGATTGAGAAATTGATCAACTCT
TCAGGATTTTCAGAGCTTTGGGCACTCCCAATAATGAAGTGTGGCCAGAAGTGGAATCTT
TACAGGACTATAAGAATACATTTCCCAATGGAAACCAGGAAGCCTAGCATCCCATGTCA
AAAACTTGGATGAAAATGGCTTGGATTTGCTCTCGAAAATGTTAATCTATGATCCAGCCA
AACGAATTTCTGGCAAAATGGCACTGAATCATCCATATTTTAATGATTTGGACAATCAGA
TTAAGAAGATGTAGCTTTCTGACAAAAGTTTCCATATGTTATGTCAACAGATAGTTGTG
TTTTTATTGTTAACTCTTGTCTATTTTTGTCTTATATATATTTCTTTGTTATCAAACCTC
AGCTGTACTTCGTCTTCTAATTTCAAAAATATAACTTAAAAATGTAAATATTCTATATGA
ATTTAAATATAATTCTGTAAATGTGAAAAAAAAAAAAAAAAAAAAA

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FIGURE 2

MEDYTKIEKIGEGTYGVVYKGRHKTTGQVVAMKKIRLESEEEGVPSTAIRESLLKELRH
PNIVSLQDVLMDQSRLYLIFEFLSMDLKKYLD SIPPGQYMDSSLVKVVT LWYRSPEVLLG
SARYSTPVDIWSIGTIFAELATKKPLFHGDSEIDQLFRIFRALGTPNNEVWPEVESLQDY
KNTFPKWKPGSLASHVKNLDENGLDLLSKMLIYDPAKRISGKMALNHPYFNDLDNQIKKM

cAMP- and cGMP-dependent protein kinase phosphorylation site.

217-220

Tyrosine kinase phosphorylation site.

9-15

N-myristoylation site.

27-32

43-48

134-139

164-169

190-195

Protein kinase domain

4-230

CTCTCGGTTCTATCATGATTGAATTGAATTCCTCCGGGGATGCTCCTCTAGAATGGAAAGTACCACACGTGTT
GGAGATGATTGGAGAAGGCTCTTTTGGGAGGGTGTACAAGGGTCTGAAGAAAATACAGTGC
TCAGGTCGTGGCCCTGAAGTTCATCCCAAATTTGGGGCGCTCAGAGAAGGAGCTGAGGAA
TTTGCAACGAGAGATTGAAATAATGCGGGGTCTGCGGCATCCCAACATTTGCGCATATGCT
TGACAGCTTTGAACTGATAAAGAGGTTGGTGGTGACAGACTATGCTGAGGAGAGCT
CTTTTCAGATCCTAGAAGATGACGGAAAACCTTCTGAAGACAGGTTTCAGGCCATTGCTGC
CCAGTTGGTGTGAGCCCTGTACTATCTGCATTCCCACCGCATCCTACACCGAGATATGAA
GCCTCAGAACATCCTCCTCGCCAAGGGTGGTGGCATCAAGCTCTGTGACTTTGGATTTCG
CCGGGCTATGAGCACCAATACAATTGGTGTGACATCCATAAAGGCACACCACTCTATAT
GTCTCCAGAGCTGGTGGAGGAGCGACCATACGACCACAGCGGACCTCTGGTCTGTTGG
CTGCATACATATATGAATGGCAGTAGGCAACCCCTCCCTTCTATGCTACAAGCATCTTTCA
GCTGGTTCAGCCTCATTCTCAAGGACCCCTGTGCGCTGGCCCTCAACCATCAGTCCCTGCTT
TAAGAACTTCCTGCAGGGACTGCTCACCAAAGACCCACGGCAGCGACTGTCTGGCCAGA
CCTCTTTATATCACCCCTTTATTTGCTGGTTCATGTCACCATAATAACTGAGCCAGCGGCC
AGATTTGGGGACCCCATTCACCAAGCGCCTACCCCCAGAATCTCAGGTCCTAAAGACGA
ACAGGCGCCATCGGTTGGCCCCCAAGGGTAATCAGTCTCGCATCTTTGACTCAGGCCTATAA
ACGCATGGCTGAGGAGGCCATGCAGAAGAAACATCAGAACACAGGACCTGCCCTTGAGCA
AGAGGACAAGACCAGCAAGGTGGCTCCTGGCACAGCCCTCTGCCAGACTCGGGGCCAC
TCCTCAGGAATCAAGCCTCCTGGCCGGGATCTTAGCCTCAGAATTGAAGAGCAGCTGGGC
TAAATCAGGACTGGAGAGGTGCCCTGACCTCGGGAAACACGGGACCCAGATTG
TGAACGAGCATCTCCGAGGAGGAGGCCAGAGGTGCTGGGCCAGCGGAGCACTGATGTAGT
GGACCTGGAAAATGAGGAGCCAGACAGTGACAATGAGTGGCAGCACCTGCTAGAGACCAC
TGAGCCTGTGCCTATTCACTGAAGGCTCCTCTCACCTTGCTGTGTAATCCTGACTTCTG
CCAGCGCATCCAGAGTCAGCTGCATGAAGCTGGAGGGCAGATCCTGAAAGGCATCTTGA
GGGTGCTTTCCCACTCTGCCCTGCTCCGGTCTGAGCAGTCTTCTCTCAGCTGCGAG
TGATTCTGTTGCTTTGATTCTTCTGCGGGGAGCGAGGGCTTCTGGGCTGCTGCTGAG
TCTACTCAGGCACAGTCAGGAGAGCAACAGCCTCCAGCAGCAATCTTGGTATGGGACCTT
CTTACAGGACCTGATGGCTGTGATTTCAGGCCTACTTTGCCTGTACCTTCAATCTGGAGAG
GAGCCAGACAAGTGACAGCCTCGAGGTGTTTTCAGGAGGCTGCCAACCTTTTCTGGACCT
GTTGGGGAACACTGCTGGCCCAACAGATGACTCTGAGCAGACTTTGCGGAGGGACAGCCT
TATGTGCTTTACTGTCTGTGCGAAGCCATGGATGGGAACAGCCGGGCCATCTCCAAAGC
CTTTTACTCCAGCTTGCTGACGACACAGCAGGTTGTCTTGGATGGGCTCCTTCATGGCTT
GACAGTTCCACAGCTCCCTGTCCACACTCCCCAAGGAGCCCCGCAAGTGAGCCAGCCACT
GCGAGAGCAGAGTGAGGATATACCTGGAGCCATTCTCTGCCCTGGCAGCCATATGAC
TGCTCCTGTGGGACTGCCGACTGCTGGGATGCCAAGGAGCAGGCTGTGTTGGCATTTGGC
AAATCAGCTAACTGAAGACAGCAGCCAGCTCAGGCCATCCCTCATCTCTGGCCTGCAGCA
TCCCATCCTGTGCCTGCACCTTCTCAAGGTTCTATACTCCTGCTGCCTTGTGAGTGAGGG
CCTGTGCCGTCTTCTGGGGCAGGAGCCCTGGCCTTGAATCCCTGTTTATGTTGATTCA
GGGCAAGGTAAAAGTAGTAGATTGGGAAGAGTCTACTGAAGTGACACTACTTCTCTC
CCTTCTGTGCTTTTCGGCTCCAAACCTGGCTTGTGGAATGGAGAAGCTAGGCAGTGACGT
TGCTACTCTCTTTACCCATTTCGCATGTGCTCTCTCTTGTGAGTGCAGCAGCCTGTCTATT
GGGACAGCTTGGTCAGCAAGGGGTGACCTTTGACCTCCAGCCCATGGAATGGATGGCTGC
AGCCACACATGCCTTGTCTGCCCTGCAGAGGTTGGTTGACTCCACAGGAGTAGTTGTGG
ATTCTATGATGGCCTCCTTATCCTTCTGTTGACGCTCCTCAGGACGGGGAAGGCTAG
CCTAATCAGGATATGTTCCAGTTTCAGAAATGGAACGCTTTGTGGCACCGCTTCTCCAT
GGTCTGAGGCTCCCCGAGGAGGCATCTGCACAGGAAGGGGAGCTTTCGCTATCCAGTCC
ACCAAGCCCTGAGCCAGACTGGACACTGATTTCCTCCCGAGGCATGGCAGCCCTGCTGAG
CCTGGCCATGGCCACCTTTACCCAGGAGCCCCAGTTATGCTGAGCTGCCTGTCCAGCA
TGGAAGTCTCTCATGTCCTGTAAGCATCTGCTTTGCCACGCTCTCTGTAATCACT
CGCGGAGGCGCCTCATGGCTCTGAGTTTCTCCTGTGCTGCTGCTCTGTCTGCCAGCT
CCTTTGCTTCCCTTTGCGCTGGACATGGATGCTGACCTCCTTATAGTTGTCTTGCCGA
CCTCAGGGACTCAGAAGTTGCAGCCCATCTGCTGCAGGTCTGCTGCTACCATCTTCCGTT
GATGCAAGTGGAGCTGCCCATCAGCCTTCTCACAGCCTGGCCCTCATGGATCCCACCTC
TCTCAACCAAGTTTGTGAACACAGTGTCTGCCCTCCCCTAGAACCATCGTCTCGTTTCTC
AGTTGCCCTCCTGAGTGACCAAGCACTGTTGACCTCCGACCTTCTCTCTGCTGGCCCA
TACTGCCAGGGTCTGTCTCTCCAGCCACTTGTCTTTATCCAAGAGCTTCTGGCTGGCTC
TGATGAATCCTATCGGCCCTGCGCAGCCTCCTGGGCCACCCAGAGAATTCGTGCGGGC
ACACACTTATAGGCTCCTGGGACACTTGCTCCAACACAGCATGGCCCTGCGTGGGGCACT
GCAGAGCCAGTCTGGACTGCTCAGCCTTCTGCTGCTTGGGCTTGGAGACAAGGATCCTGT
TGTGCGGCTGACGTGCCAGCTTTGCTGTGGCAATGCAGCTTACAGGCTGTCTCTCTGGG
ACCTGCCCTGGCAGCTGCAGTGCCAGTATGACCCAGCTGCTTGGAGATCCTCAGGCTGG
TATCCGGCGCAATGTTGCATCAGCTCTGGGCAACTTGGGACCTGAAGGTTTGGGAGAGGA

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FIGURE 3B

GCTGTTACAGTGCGAAGTACCCAGCGGCTCCTAGAAATGGCATGTGGAGACCCCAGCC
AAATGTGAAGGAGGCTGCCCTCATTGCCCTCCGGAGCCTGCAAAGAGCCTGGCATCCA
TCAGGTACTGGTGTCCCTGGGTGCCAGTGAGAACTATCCTTGCTCTCTCTGGGGAATCA
GTCAGTGCACACAGCAGTCCTAGGCCTGCCTCTGCCAAACACTGCAGGAACTCATTCA
CCTCCTGAGGCCAGCCATAGCATGTGAAGCTTGGCCGCCATGGCCC

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FIGURE 4A

MEKYHVLEMIGEGSFGRVYKGRRKYSAQVVALKFIPKLGRSEKELRNLOREIEIMRGLRH
 PNIVHMLDSFETDKEVVVVTDYAEGELFQILEDDGKLPEDQVQAIAAQLVSALYYLHSHR
 ILHRDMKPKQNILLAKGGGIKLCDFGFARAMSTNTMVLTSIKGTPLYMSPELVEERPYDHT
 ADLWSVGCILYELAVGTPPFYATSIFQLVSLILKDPVRWPSTISPCFKNFLQGLLT KDPR
 QRLSWPDLLYHPFIAGHVTTIITEPAGPDLGTPFTSRLPPELQVLKDEQAHRLAPKGNQSR
 ILTQAYKRMAEEAMQKKHONTGPALQEDKTSKVAPGTAPLPRLGATPQESSLLAGILAS
 ELKSSWAKSGTG EVPSAPRENRTTPDCERAFPEERPEVLGQRSTDVVDLENEEPDS DNEW
 QHLETTEPVPIQLKAPLTLLCNPDFCQRIQS QLHEAGGQILKGILEGASHILPAFRVLS
 SLLSSCSDSVALYSFCREAGLPGLLLSLLRHSQESNSLQQQSWYGTFLQDLMAVIQAYFA
 CTFNLERSQTSDSLQVFOEAAANFLDLLGKLLAQPDSEQTLRRDSL MCF TVLCEAMDGN
 SRAISKAFYSSLLTTQQVVL DGLLHGLTVPQLPVHTPQGAPQVSQPLREQSEDI PGAISS
 ALAAICTAPVGLPDCWDAKEQVCWHLANQLTEDSSQLRPSLISGLQHPILCLHLLKVLYS
 CCLVSEGLCRLLGQEPLALESLEFMLIQGKV KVV DWEESTEVTL YFLSLLV FRLQNLPCGM
 EKLGS DVATLFT HSHVSVLSAAACLLGQLGQQGVTFDLQPM EWMAAATHALSAPAEVRL
 TPPGSCGFYDGLLILLQLLTEQGKASLIRDMSSSEMWT VLVHHRFSMVLRLPEEASAQEG
 ELSLSSPPSPEPDWTLIS PQGMAALLSLAMATFTQEPQLCLSCLSQHGSILMSILKHL LC
 PSFLNQLRQAPHGSEFLPVVVL SVCQLLCFPFALDMDADLLIVVLADLRDSEVA AHL LQV
 CCYHLPLMQVELPISLLTRLALMDPTSLNQFVNTVSASPTIVSFLSVALLSDQPLLTSD
 LLSLLAHTARVLSPSHLSFIQELLAGSDES YRPLRSLLGHPENS VRAHTYRL LGHLLQHS
 MALRGALQSQSGLLSLLLLGLGDKDPVVRCSASFVGNAA YQAGPLGPALAAAVPSMTQL
 LGDPQAGIRRNVASALGNLGP EGLGEELLQCEVPQRLL EMACGDPQPNVKEAALIALRSL
 QQEPGIHQVLVSLGASEKLSLLSLGNQSLPHSSPRPASAKHCRKLIHLLRPAHSM

N-glycosylation site.

297-300
 381-384
 1286-1289

Glycosaminoglycan attachment site.

369-372

cAMP- and cGMP-dependent protein kinase phosphorylation site.

23-26
 583-586

N-myristoylation site.

138-143
 270-275
 356-361
 400-405
 464-469
 503-508
 599-604
 622-627
 656-661
 671-676
 784-789
 1106-1111
 1145-1150
 1207-1212

Amidation site.

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FIGURE 4B

Leucine zipper pattern.

769-790
987-1008

Serine/Threonine protein kinases active-site signature.

121-133

Protein kinase domain
1-294

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FIGURE 5A

CAGAGCAGGGCGAGAGCCGATCAGCGGATCACCGAGTCTCGCCAGGTGGTGGAGCTGGCA
GTGAAGGAGCACAAGGCTGAGATTCTCGCTCTGCAGCAGGCTCTCAAAGAGCAGAAGCTG
AAGGCCGAGAGCCTCTCTGACAAGCTCAATGACCTGGAGAAGAAGCATGCTATGCTTGAA
ATGAATGCCCGAAGCTTACAGCAGAAGCTGGAGACTGAACGAGAGCTCAAACAGAGGCTT
CTGGAAGAGCAAGCCAAATTACAGCAGCAGATGGACCTGCAGAAAAATCACATTTTCCGT
CTGACTCAAGGACTGCAAGAAGCTCTAGATCGGGCTGATCTACTGAAGACAGAAAGAAGT
GACTTGGAGTATCAGCTGGAAAACATTACAGGTTCTCTATTCTCATGAAAAGGTGAAAATG
GAAGGCACTATTTCTCAACAAACCAAACTCATTGATTTTCTGCAAGCCAAAATGGACCAA
CCTGCTAAAAAGAAAAGGTTCTCTGCAGTACAATGAGCTGAAGCTGGCCCTGGAGAAG
GAGAAAGCTCGCTGTGCAGAGCTAGAGGAAGCCCTTCAGAAGACCCGCATCGAGCTCCGG
TCCGCCCGGGAGGAAGCTGCCACCGCAAAGCAACGGACCACCCACACCCATCCACGCCA
GCCACCGCGAGGCAGCAGATCGCCATGTCTGCCATCGTGCCTGCGCCAGAGCACCAGCCC
AGTGCCATGAGCCTGTGGCCCCGCCATCCAGCCGCAGAAAGGAGTCTTCAACTCCAGAG
GAATTTAGTCGGCGTCTTAAGGAACGCATGCACCACAATATTCTCACCAGATTCAACGTA
GGACTGAACATGCGAGCCCAAAGTGTGCTGTGTCTGGATAACCGTGCATTTGGACGC
CAGGCATCCAAATGTCTCGAATGTGAGGTGATGTGTACCCCAAGTGCTCCACGTGCTTG
CCAGCCACCTGCGGCTTGCTGTGAATATGCCACACACTTCACCGAGGCTTCTGCCGT
GACAAATGAAGTCCCCAGGTCTCCAGACCAAGGAGCCAGCAGCAGCTTGACCTGGAA
GGGTGGATGAAGGTGCCAGGAATAACAAACGAGGACAGCAAGGCTGGGACAGGAAGTAC
ATTGTCTGGAGGGATCAAAGTCTCATTTATGACAATGAAGCCAGAGAAGCTGGACAG
AGGCCGCTGGAAGAATTTGAGCTGTGCCCTCCCGACGGGGATGTATCTATTATGCTGCC
GTTGGTGCTTCCGAAGTCCGAAATACAGCCAAAGCAGATGTCCATACATACTGAAGATG
GAATCTCACCCGCACACCACCTGCTGGCCCCGGGAGAACCCTCTACTTGCTAGCTCCAGC
TTCCCTGACAAACAGCGCTGGGTACCCGCTTAGAATCAGTTGTGCGAGGTGGGAGAGTT
TCTAGGAAAAAGCAGAAGCTGATGCTAAAGTCTTGGAACTCCCTGCTGAAACTGGAA
GGTGATGACCGTCTAGACATGAAGTGCACGCTGCCCTTCAGTGACCAGGTGGTGTGGTG
GGCACCAGGAAGGGCTCTACGCCCTGAATGTCTTGAAAACTCCCTAACCCTATGTCCCA
GGAATTTGAGCAGTCTTCCAAATTTATATTTATCAAGGACCTGGAGAAGCTACTCATGATA
GCAGGAGAAGAGCGGGCACTGTGTCTTGTGGACGTGAAGAAAGTGAACAGTCCCTGGCC
CAGTCCACCTGCTGCCCCAGCCCCGACATCTCACCAACATTTTGAAGCTGTCAAGGGC
TGCCACTTGTGTTGGGGCAGGCAAGATTGAGAACGGGCTCTGCATCTGTGCAGCCATGCCC
AGCAAAGTCGTCTTCTCCGCTACAACGAAAACCTCAGCAAATACTGCATCCGGAAAGAG
ATAGAGACCTCAGAGCCCTGCAGCTGTATCCACTTCACCAATTACAGTATCCTCATTTGA
ACCAATAAATTTACGAAATCGACATGAAGCAGTACACGCTCGAGGAATTCCTGGATAAG
AATGACCATTTCTTGGCACCTGCTGTGTTTGGCGCTCTTCCAACAGCTTCCCTGTCTCA
ATCGTGCAGGTGAACAGCGCAGGGCAGCGAGAGGAGTACTTGCTGTGTTTCCACGAATTT
GGAGTGTTCGTGGATTCTTACGGAAGACGTAGCCGCACAGACGATCTCAAGTGGAGTCGC
TTACCTTTGGCCTTTGCTTACAGAGAACCCATCTGTTTGTGACCCACTTCAACTCACTC
GAAGTAATTGAGATCCAGGCACGCTCCTCAGCAGGGACCCCTGCCGAGCGTACCTGGAC
ATCCCGAACCCGCGCTACCTGGGCCCTGCCATTTCTCAGGAGCGATTACTTTGGCGTCC
TCATACCAGGATAAATTAAGGGTCATTTGCTGCAAGGGAAACCTCGTGAAGGAGTCCGGC
ACTGAACACCACCGGGGCCCCGTCCACCTCCCGCAGCAGCCCCAACAAAGCGAGGCCACCC
ACGTACAACGAGCAGATCACCAAGCGGTGGCCCTCCAGCCAGCGCCGCCCCGAAGGCCCC
AGCCACCCGCGAGGCCAAGCACACCCACCGCTACCGCGAGGGGCGGACCCGAGCTGCGC
AGGGACAAGTCTCTGGCCGCCCTTGGAGCGAGAGAAGTCCCCCGCCGGATGCTCAGC
ACGCGGAGAGAGCGGTCCCCGGGAGGCTGTTTGAAGACAGCAGCAGGGGCGCGGTGCCT
GCGGGAGCCGTGAGGACCCCGCTGTCCAGGTGAACAAGGTCTGGGACCACTTTCAGTA
TAAATCTCAGCCAGAAAAACCAACTCCTCATCTTGATCTGCAGGAAAAACCAAACACAC
TATGGAATCTGCTGATGGGGACCCAAGCGCCACGTGCTCAGCCACCCCTCTGGCTCAGC
GGGGCCCCAGACCCACTCGGCACGGACACCCCTGTCTCAGGAGGGGCGAGGTGGCTGAGG
CTCTTCGGAGCTGTGACGCCCCGGTGCCCTGCCCTGGGCACCTCCCTGCAGTCATCTCTTT
GCACTTTGTTACTCTTTCAAAGCATTACAAACTTTTGTACCTAGCTCTAGCCTGTACCA
GTTAGTTTCATCAAAGGAACCAACCGGGATGCTAACAAACATGGTTAGAATCCTAATT
AGCTACTTTAAGATCCTAGGATTGGTTGGTTTTTCTTTTTTTTTTCTTTTGTCTTTT
CTTTTTTTTTTTTTTTTTTAAGACAACAGAATTCCTTAATAGATTTGAATAGCGACGTATT
TCCTGTTGTAGTCATTTTTAGCTCGACCACATCATCAGGTCTTGCCACCGAGGCATAGT
GTAGAACAGTCCCGGTCACTTGGCCAACCTCCCGCAGCCAAGTAGGTTTCATCCTTGTTC
TGTTCAATTCATAGATGGCCCTGCTTTCCCCAGGGTGACATCGTAGCCAAATGTTTACT
GTTTTCAATGCTTTTATGGCCTTGACGACTTCCCTCCACAGCTGAGAATGTATGGA
GTTTCATCGGGGCTCAGCTCGGAGGCGAGTACTTGGGGCCAAGGGACCTCGAGACGCTTT
CCTTCCCCACCCCCCAGCGTCATCTCCCCAGCCTGCTGTTCCCGCTTTCCATATAGCTTT
GGCCAGGAAGCATGCAATAGACTTGCTCGGAGCCAGCACTCCTGGGTCTCGGGTTCGG

GGAGGGGACGGGGGACCCACTTCCTTGTCTGTGACGGCGTGTGTGTTCCCACTCTGGGA
TGGGGAAGAGGCCCGTCGGGAGTTCTGCATGGCAGTTCACTGCATGTGCTGCCCCCTTGG
GTTGCTCTGCCAATGTATTAATACCATCCCATAGCTCCTGCCAAATCGAGACCCCTGAC
GACTTGGCCGACTAAGTGGCCACCAAGCTGCAGTCTGTAGCACTGAACAAACAAAAAAC
AAAACGCTCAAGCCTTACGACACAGAGAAGGATTTACGAAACACCACCACTCCCACTCAG
GTCCCCCTCCAAACTTCACACTTCCCTGCCTGCAGAGGATGACTCTGTTACACCCCAATCC
AGCGCGGTTCTACCCACGAAACTGTGACTTTCCAAATGAGCCTTTCCTAGGGCTAGAC
CTAAGACCGAGGAAGTTTGAGAAAGCAGCGCAGCTCAACTCTTCCAGCTCCGCCAGGGTT
GGGAAGTCCTTAGGTGCAGTGCAGTCCCACTGGGTCTGCGGACCCCTCCTATTAGAGTAC
GAAATTCCTGGCAACTGGTATAGAACCAACCTAGAGGCTTTGCAGTTGGCAAGCTAACTC
GCGGCCTTATTTCTGCCTTTAACTCTCCACAAGGCATCTGTTGCTTTGGGTCTCCACGA
CTCTTAGGCCCCGCTCAACAACCCAGGCACCTCCTAGGTAGGCTCAAAGGTAGACCCGTT
TCCACCGCAGCAGGTGAACATGACCGTGTTTTCAACTGTGTCCACAGTTTCAGATCCCTTT
CCAGATTGCAACCTGGCCCTGCATCCGAGTCTCTCTGCTCGTGTCTTAACCTAAGTGCT
TTCTTGTTTGAACGCTTACAACCTCCATGTGGTAGCTCCTTTGGCAATGTCTGTCTG
TGGCGTTTTATGTGTTGCTTGGAGTCTGTGGGGTCGTACTCCCTCCCTCCCGTCCCCAG
GGCAGATTTGATTGAATGTTTGCTGAAGTTTTGTCTCTTGGTCCACAGTATTTGGAAAGG
TCACTGAAAATGGGTCTTTAGTCTTTGGCATTTCATTTAGGATCTCCATGAGAAATGGG
TTCTTGAGCCCTGAAATGTATATTGTGTCTCATCTGTGAAGCTTTCTGCTATATA
GAAGTACTCAAAGACTGTACATATTTACAAGAACTTTATATTGTAAGAAAAAAG
AGGAAATTGAATTGGTTTCTACTTTTTTATTGTAAGAGGTGCATTTTTTCAACACTTACTT
TTGGTTTCAATGGTGGTAGTTGTGGACAGCCATCTTCACTGGAGGTGGGGAGCTCCGTG
TGACCACCAAGATGCCAGCAGGATATACCGTAACACGAAATGCTGTCAAAGCTTATTA
GCATCAATCAAGATTCTAGGTCTCCAAAAGTACAGGCTTTTTCTTCACTTTTATTA
TCAAGACGAGGAAGAGAACACAAGAAATGATTCAAGATCCACTTGAGAGGAATGAACCT
TGTTGTTGAACAATTAGTGAATAAAGCAATGATCTAACT

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FIGURE 6

MLEMNARSLQOKLETERELKQRLLEEQAQLQQQMDLQKNHIFRLTQGLQEALDRADLLKT
 ERSLEYQLENIQVLYSHEKVMEGTISQOTKLIDFLQAKMDQPAKKKKVPLQYNELKLA
 LEKEKARCAELEELQKTRIELRSAREEAHRKATDHPHPSTPATARQQIAMSIVRSPE
 HQPSAMSLAPPSSRRKESSTPEEFSRRLKERMHHNIPHRFNVGLNMRATKCAVCLDTVH
 FGRQASKCLECQVMCHPKCSTCLPATCGLPAEYATHFTEAFCDKMNSPGLQTKEPSSSL
 HLEGWMKVPRNNKRGQQGWDKRYIVLEGSKVLIYDNEAREAGQRPVEEFELCLPDGDVSI
 HGAVGASELANTAKADVPIILKMESHPTTCWPGRTLYLLAPSFDPKQRWVTALESVVAG
 GRVSREKAEADAKLLGNSLLKLEGDDRLDMNCTLPFSDQVVLVGTEEGLYALNVLKNSLT
 HVPGIGAVFQIYIIKDLEKLLMIAGEERALCLVDVKVKQSLAQSHLPAQPDISPNIFFEA
 VKGCHLFGAGKIENGLCICAAMPSKVILRYNENLSKYCIRKEIETSEPCSCIHFTNYSI
 LIGTNKFYEIDMKQYTLEEFLDKNDHSLAPAVFAASSNSFPVSIVQVNSAGQREEYLLCF
 HEFGVFVDSYGRRSRTDDLKWSRLPLAFAYREPYLFVTHFNSLEVIEIQARSSAGTPARA
 YLDIPNPRYLGPATSSGAIYLAASSYQDKLRVICCKGNLVKESGTEHHRGPSTSRSSPNKR
 GPPTYNEHITKRVASSPAPPEGSPHPREPSTPHRYREGRTELRRDKSPGRPLEREKSPGR
 MLSTRRERSPGRLFEDSSRGRLPAGAVRTPLSQVNVWDQSSV

N-glycosylation site.

451-454
 574-577
 597-600

cAMP- and cGMP-dependent protein kinase phosphorylation site.

152-155
 196-199

N-myristoylation site.

47-52
 362-367
 420-425
 464-469
 555-560

Amidation site.

670-673

Carbamoyl-phosphate synthase subdomain signature 2.

1-8

CNH domain
 448-745

PH domain
 300-419

Phorbol esters/diacylglycerol binding domain
 219-267

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FIGURE 7

AAAGGCCTGCAGCAGGACGAGGACCTGAGCCAGGAATGCAGGATGGCGGCGGTGAAGAAAG
GAAGGGGGTGCTCTGAGTGAAGCCATGTCCCTGGAGGGAGATGAATGGGAAGTGAAGTAAA
GAAAATGTACAACCTTTAAGGCAAGGGCGGATCATGTCCACGCTTCAGGGAGCACTGGCA
CAAGAATCTGCCTGTAACAATACTCTTCAGCAGCAGAAACGGGCATTTGAATATGAAATT
CGATTTTACACTGGAATGACCTCTGGATGTTTGGGATAGGTATATCAGCTGGACAGAG
CAGAACATCTCTCAAGGTGGGAAAGAGAGTAATATGTCAACGTTATTAGAAAAGAGCTGTA
GAAGCACTACAAGGAGAAAACGATATTATAGTGATCCTCGATTTCTCAATCTCTGGCTT
AAATTAGGGCGTTTATGCAATGAGCCTTTGGATATGTACAGTTACTTGCACAACCAAGGG
ATTGGTGTTTTCACTTGCTCAGTTCTATATCTCATGGGCAGAAGAATATGAAGCTAGAGAA
AACTTTAGGAAAGCAGATGCGATATTTAGGAAGGGATTCAACAGAAGGCTGAACCACTA
GAAAGACTACAGTCCCAGCACCGACAATTCCAAGCTCGAGTGCTCTCGGCAAACTCTGTTG
GCACTTGAGAAAGAAGAAGAGGAGGAAGTTTGTAGTCTTCTGTACCACAACGAAGCACA
CTAGCTGAACATAAGAGCAAAGGGAAAAAGACAGCAAGAGCTCCAATCATCCGTGTAGGA
GGTGCTCTCAAGGCTCCAAGCCAGAACAGAGGACTCCAAAATCCATTTCCCTCAACAGATG
CAAAATAATAGTAGAATTACTGTTTTTGTATGAAAATGCTGATGAGGCTTCTACAGCAGAG
TTGTCTAAGCCTACAGTCCAGCCATGGATAGCACCCCCCATGCCAGGGCCAAAGAGAAT
GAGCTGCAAGCAGGCCCTTGGAACACAGGCAGGTCTTGGAACACAGGCCCTCGTGGCAAT
ACAGCTTCACTGATAGCTGTACCGCTGTGCTTCCAGTTTCACTCCATATGTGGAAGAG
ACTGCACAACAGCCAGTTATGACACCATGTAAAATTGAACCTAGTATAAACCCACATCCTA
AGCACCAGAAAGCCTGGAAAGGAAGAGGAGATCCTCTACAAAGGGTTAGAGCCATCAG
CAAGCGTCTGAGGAGAAGAAAGAGAAGATGATGTATTGTAAGGAGAAGATTTATGCAGGA
GTAGGGGAATTCTCCTTTGAAGAAATTCGGGCTGAAGTTTCCGGAAGAAATTAAGAGAG
CAAAGGGAGCCGAGCTATTGACCAGTGTCAGAGAAGAGAGCAGAAATGCAGAAACAGATT
GAAGAGATGGAGAAGAAGCTAAAAGAAATCCAACTACTCAGCAAGAAAGAACAGGTGAT
CAGCAAGAAGAGACGATGCTTACAAAGGAGACAACATAAAGTGCATAATGCTTCCGAGTCT
CAGAAAATACCAGGAATGACTCTATCCAGTTCTGTTTGTCAAGTAACTGTTGTGCCAGA
GAACTTCACTTCCGAGAACATTTGGCAGGAACAACCTCATTCTAAAGGTCCAGTGTA
CCTTTCTCCATTTTGTATGAGTTTCTTCTTTTCAAGAAAGAAATAAAGTCTCTGCA
GATCCCCCAGGTTTGTCTCAACGAAGACCCCTTGAGTTCTCAAAACCTCAGAAAGC
ATCAGCTCAAAATGAAGATGTGTCTCCAGATGTTTGTGATGAATTTACAGGAATTGAACCC
TTGAGCGAGGATGCCATTATCACAGGCTTCAGAAATGTAACAATTTGTCTAACCAGAA
GACACTTGTGACTTTGCCAGAGCAGCTCGTTTTGTATCCACTCCTTTTCATGAGATAATG
TCCTTGAAGGATCTCCCTTCTGATCCTGAGAGACTGTTACCGGAAGAAGATCTAGATGTA
AAGACCTCTGAGGACAGCAGACTTGTGGCACTATCTACAGTCAGACTCTCAGCATC
AAGAAGCTGAGCCCAATTATTGAAGACAGTCGTGAAGCCACACACTCCTCTGGCTTCTCT
GGTCTTCTGCCTCGGTTGCAAGCACCTCCTCCATCAAATGTCTTCAAATTCCTGAGAAA
CTAGAATTACTAATGAGACTTCAGAAAACCTACTCAGTCACCATGGTGTTCACAGTAT
CGCAGACAGCTACTGAAGTCCCTACCAGAGTTAAGTGCTCTGCAGAGTTGTGTATAGAA
GACAGACCAATGCTTAAGTTGGAATTTGAGAAGGAAATGAATTAGGTAATGAGGATTAC
TGCATTAAACGAGAATACCTAATATGTGAAGATTACAAGTTATTCTGGGTGGCGCCAAGA
AACTCTGCAGAATTAACAGTAATAAAGGTATCTTCTCAACCTGTCCCATGGGACTTTTAT
ATCAACCTCAAGTTAAAGGAACGTTTAAATGAAGATTTTGTATCATTTTTTGCAGCTGTTAT
CAATATCAAGATGGCTGTATTGTTTGGCACCAATATATAAAGTCTTACCCCTCAGGAT
CTTCTCCAACACAGTGAATATATTACCCATGAAATAACAGTGTTGATTATTTATAACCTT
TTGACAATAGTGGAGATGCTACACAAAGCAGAAATAGTCCATGGTGACTTGAGTCCAAGG
TGTCTGATTCTCAGAAACAGAATCCACGATCCCTATGATTGTAACAAGAACAATCAAGCT
TTGAAGATAGTGGACTTTTCTACAGTGTTGACCTTAGGGTGCAGCTGGATGTTTTTACC
CTCAGCGGCTTTCCGACTGTACAGATCCTGGAAGGACAAAAGATCCTGGCTAACTGTTCT
TCTCCCTACCAGGTAGACCTGTTTGGTATAGCAGATTTAGCACATTACTATTGTTCAAG
GAACACCTACAGGTCTTCTGGGATGGGTCTTCTGGAACCTTAGCCAAAATATTTCTGAG
CTAAAAGATGGTGAATTGTGGAATAAATCTTTGTGCGGATTCTGAATGCCAATGATGAG
GCCACAGTGTCTGTTCTTGGGGAGCTTGCAGCAGAAATGAATGGGGTTTTTGCAGCTACA
TTCCAAAGTCACTGAACAAAGCCTTATGGAAGGTAGGGAAGTTAACTAGTCTGGGGCT
TTGCTCTTTTCACTGAGCTAGGCAATCAAGTCTCACAGATTGCTGCCTCAGAGCAATGGTT
GTATTGTGGAACACTGAACTGTATGTGCTGTAATTTAATTTAGGACACATTTAGATGCA
CTACCATTGCTGTTCTACTTTTTTGGTACAGGTATATTTTGCAGTCACTGATATTTTTTAT
ACAGTGATATACTTACTCATGGCCTTGTCTAACTTTTTGTGAAGAACTATTTTATTCTAAA
CAGACTCATTACCAATGGTTACCTTGTATTATTAACCCATTTGTCTCTACTTTTCCCTGTA
CTTTTCCCAATTTGTAATTTGTAAAATGTTCTCTTATGATCACCATGATTTTGTAAATAA
TAAATAGTATCTGTTAAAAA

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FIGURE 8

MAAVKKEGGALSEAMSLEGDEWELSKENVQPLRQGRIMSTLQGALAQESACNNTLQQQKR
 AFEYEIRFYTGNDPLDVWDRIYISWTEQNYPQGGKESNMSTLLERAVEALQGEKRYYS DPR
 FLNLWLKLGRLCNEPLDMYSYLHNQGIGVSLAQFYISWAEYEARENFRKADAI FQEGIQ
 QKAEPLERLQSQHRQFQARVSRQTLLEKEEEEEVFESSVPQRSTLAEKSKGKKTARA
 PIIRVGGALKAPSONRGLQNPFPQMQNNSRITVFDENADEASTAELSKPTVQPWIAPPM
 PRAKENELQAGPWNTGRSLEHRPRGNTASLIAVPAVLPSFTPYVEETAQQPVMT PCKIEP
 SINHILSTRKPGKEEGDPLQRVQSHQQASEEKKEKMMYCKEKIYAGVGFEFSFEEIRAEVF
 RKKLKEQREAEELLTSAEKRAEMQKQIEEMEKKLKEIQTTQQERTGDQQEETMPTKETTKL
 QIASESQKIPGMTLSSSVCQVNCCARETSLAENIWQEQPHSKGPSVPFSIFDEFLLSEKK
 NKSPPADPPRVLAQRRPLAVLKTSESITSNEDVSPDVCDEFTGIEPLSEDAIITGFRNVT
 ICPNPEDTCDFARAARFVSTPFHEIMSLKDLPSDPERLLPEEDLDVKTSEDQQTACGTIY
 SQTLSIKKLSPIIEDSREATHSSGFGSSASVASTSSIKCLQIPEKLELTNETSENPTQS
 PWCSQYRRQLLKSLPELSASAELCIEDRPM PKLEIEKEIELGNEDYCIKREY LICEDYKL
 FWVAPRNSAELTVIKVSSQPV PWFDFYINLKLKERLNEDFDHFCSCYQYQDGCIVWHQYIN
 CFTLQDLLQHSEYITHEITVLI IYNLLTIVEMLHKA EIVHGDLSPRCLILRNRIHDPYDC
 NKNNQALKIVDFSYSDLRVQLDVFTLSGFRTVQILEGQKILANCSSPYQVDLFGIADLA
 HLLLKFKEHLQVFDGSEFWKLSQNI SELKD GELWNKFFVRILNANDEATVSVLGELAAEMN
 GVFDTTTFQSHLNKALWKVGKLTSPGALLFQ

N-glycosylation site.

52-55
 97-100
 268-271
 598-601
 711-714
 944-947
 983-986

cAMP- and cGMP-dependent protein kinase phosphorylation site.

667-670

Tyrosine kinase phosphorylation site.

908-914

N-myristoylation site.

8-13
 92-97
 146-151
 148-153
 325-330
 491-496
 657-662
 687-692
 1021-1026

Amidation site.

233-236

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FIGURE 9

GGAAGACTTGGGTCTTGGGTGCGCAGGTGGGAGCCGACGGGTGGGTAGACCGTGGGGGAT
ATCTCAGTGGCGGACGAGGACGGCGGGGACAAGGGGCGGCTGGTCCGAGTGGCGGAGCGT
CAAGTCCCCTGTGCGTTCCCTCCGTCCCTGAGTGTCTTGGCGCTGCCTTGTGCCCGCCCA
GCGCCTTTGTCATCCGCTCCTGGGCACCGAGGCGCCCTGTAGGATACTGCTTGTACTTAT
TACAGCTAGAGGCATCATGACCGATCTAAAGAAAAGTGCATTTACGGACCTGTTAAGGC
TACAGCTCCAGTTGGAGGTCCAAAACGTGTTCTCGTGACTCAGCAAATTCCTTGTGAGAA
TCCATTACCTGTAAATAGTGGCCAGGCTCAGCGGGTCTTGTGTCCTTCAAATTCCTCCCA
GCGCGTTCCCTTTGCAAGCACAAAAGCTTGTCTCCAGTCACAAGCCGGTTTCAAGATCAGAA
GCAGAAGCAATTGCAGGCAACCAAGTGTACCTCATCTGTCTCCAGGCCACTGAATAACAC
CCAAAAGAGCAAGCAGCCCCCTGCCATCGGCACCTGAAAATAATCTGAGGAGGAAGTGGC
ATCAAAACAGAAAAATGAAGAATCAAAAAAGAGGCAGTGGGCTTTGGAAGACTTTGAAAT
TGGTCGCCCTCTGGGTAAAGGAAAGTTTGGTAATGTTTATTTGGCAAGAGAAAAGCAAAG
CAAGTTTATTCTGGCTCTTAAAGTGTATTTAAAGCTCAGCTGGAGAAAAGCCGGAGTGGGA
GCATCAGCTCAGAAGAGAAGTAGAAATACAGTCCACCTTCGGCATCCTAATATTCTTAG
ACTGTATGGTTATTTCCATGATGCTACCAGAGTCTACCTAATTCCTGGAATATGCACCACT
TGAACAGTTTATAGAGAACTTCAGAACTTTCAAAGTTTGATGAGCAGAGAACTGCTAC
TTATATAACAGAATTGGCAAATGCCCTGTCTTACTGTGCTATTGGAAGAGAGTTATTCATAG
AGACATTAAGCCAGAGAACTTACTTCTTGGATCAGCTGGAGAGCTTAAATTCAGATTTT
TGGGTGGTCAGTACATGCTCCATCTTCCAGGAGGACCACTCTCTGTGGCACCCTGGACTA
CCTGCCCCCTGAAATGATTGAAGGTCGGATGCATGATGAGAAGGTGGATCTCTGGAGCCT
TGGAGTTCTTTGCTATGAATTTTTAGTTGGGAAGCCTCCTTTTGAGGCAAACACATACCA
AGAGACCTACAAAAGAATATCACGGGTGAATTCACATTCCCTGACTTTGTAACAGAGGG
AGCCAGGGACCTCATTTCAAGACTGTTGAAGCATAATCCCAGCCAGAGGCCAATGCTCAG
AGAAGTACTTGAACACCCCTGGATCACAGCAAATTCATCAAAACCATCAAATTGCCAAAA
CAAAGAATCAGCTAGCAAACAGTCTTAGGAATCGTGACGGGGGAGAAATCCTTGAGCCAG
GGCTGCCATATAACCTGACAGGAACATGCTACTGAAGTTTATTTTACCATTGACTGCTGC
CCTCAATCTAGAACGCTACACAAGAAATATTTGTTTTACTCAGCAGGTGTGCCTTAACCT
CCCTATTCAAGAAAGCTCCACATCAATAAACATGACACTCTGAAGTGAAAGTAGCCACGAG
AATTGTGCTACTTATACTGGTTCATAATCTGGAGGCAAGGTTGACTGCAGCCGCCCGGT
CAGCCTGTGCTAGGCATGGTGTCTTCACAGGAGGCAAATCCAGAGCCTGGCTGTGGGGAA
AGTGACCACTCTGCCCTGACCCCGATCAGTTAAGGAGCTGTGCAATAACCTTCCTAGTAC
CTGAGTGAGTGTGTAACCTTATTGGGTGGCGAAGCCTGGTAAAGCTGTTGGAATGAGTAT
GTGATTCTTTTTAAGTATGAAAATAAAGATATATGTACAGACTTGTATTTTTCTCTGGT
GGCATTCTTTTAGGAATGCTGTGTGCTGTCCGGCACCCCGGTAGGCCTGATTGGGTTTC
TAGTCTCTCTTAACCACTTATCTCCCATATGAGAGTGTGAAAAATAGGAACACGTGCTCT
ACCTCCATTTAGGGATTTGCTTGGGATACAGAAGAGGCCATGTGTCTCAGAGCTGTTAAG
GGCTTATTTTTTTAAACATTGGAGTCATAGCATGTGTGTAACTTTAAATATGCAAATA
AATAAGTATCTATGTCTAAAAA

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FIGURE 10

MDRSKENCISGPVKATAPVGGPKRVLVTQQIPCONPLPVNSGQAQRVLCPSNSSQRVPLQ
AQKLVSSHKPVQNKQKQLQATSVPHFVSRPLNNTQKSKQPLPSAPENNPEEELASKQKN
EESKKRQWALEDFEIGRPLGKGFVYLAAREKQSKFILALKVLFKAQLEKAGVEHQLRR
EVEIQSHLRHPNLRLYGYFHDATRVYLILEYAPLGTVYRELQKLSKFDEQRTATYITEL
ANALSYCHSKRVIHRDIKPENLLLGSAGELKIADFGWSVHAPSSRRTTLCGTLDYLPPEM
IEGRMHDEKVDLWSLGVLCYEFLVGKPPFEANTYQETYKRISRVEFTFPDFVTEGARDLI
SRLLKHNPSQRPMLEVLHPWITANSSKPSNCONKESASKQS

N-glycosylation site.

52-55
93-96
386-389

cAMP- and cGMP-dependent protein kinase phosphorylation site.

285-288
339-342

Tyrosine kinase phosphorylation site.

326-334

Serine/Threonine protein kinases active-site signature.

252-264

Protein kinase domain
133-383

14/46

FIGURE 11

GGCCGGACAGTCCGCCGAGGTGCTCGGTGGAGTCATGGCAGTGCCCTTTGTGGAAGACTG
GGACTTGGTGCAAACCTGGGAGAAGGTGCCTATGGAGAAGTTCAACTTGCTGTGAATAG
AGTAACTGAAGAAGCAGTCGCAGTGAAGATTGTAGATATGAAGCGTGCCGTAGACTGTCC
AGAAAATATTAAGAAAGAGATCTGTATCAATAAAATGCTAAATCATGAAAATGTAGTAAA
ATTCTATGGTACACAGGAGAGAAGGCAATATCCAATATTTATTTCTGGAGTACTGTAGTGG
AGGAGAGCTTTTGGACAGAATAGAGCCAGACATAGGCATGCCTGAACCAGATGCTCAGAG
ATTCTTCCATCAACTCATGGCAGGGGTGGTTTATCTGCATGGTATTGGAATAACTCACAG
GGATATTAAACCAGAAAATCTTCTGTTGGATGAAAGGGATAACCTCAAAATCTCAGACTT
TGGCTTGGCAACAGTATTTCCGTATAATAATCGTGAGCGTTTGTGGAACAAGATGTGTGG
TACTTTACCATATGTTGCTCCAGAACTTCTGAAGAGAAGAGAATTTCATGCAGAACCAGT
TGATGTTTGGTCCGTGTGGAATAGTACTTACTGCAATGCTCGCTGGAGAATTGCCATGGGA
CCAACCCAGTGACAGCTGTCAGGAGTATTCTGACTGGAAAGAAAAAAAACATAACCTCAA
CCCTTGGAAAAAATCGATTCTGCTCCTCTAGCTCTGCTGCATAAAATCTTAGTTGAGAA
TCCATCAGCAAGAATTACCATTCCAGACATCAAAAAAGATAGATGGTACAACAAACCCCT
CAAGAAAGGGGCAAAAAGGCCCGAGTCACCTTCAGGTGGTGTGTCAGAGTCTCCAGTGG
ATTTTCTAAGCACATTCAATCCAATTTGGACTTCTCTCCAGTAAACAGTGCTTCTAGTGA
AGAAAATGTGAAGTACTCCAGTTCTCAGCCAGAACCCCGCACAGGTCTTTCCTTATGGGA
TACCAGCCCCCTCATACATTGATAAATTGGTACAAGGGATCAGCTTTTCCCAGCCCACATG
TCCTGATCATATGCTTTTGAATAGTCAGTTACTTGGCACCCAGGATCCTCACAGAACCC
CTGGCAGCGGTTGGTCAAAAGAATGACACGATTCTTTACCAAATTGGATGCAGACAAATC
TTATCAATGCCTGAAAGAGACTTGTGAGAAGTTGGGCTATCAATGGAAGAAAAGTTGTAT
GAATCAGGTTACTATATCAACAACCTGATAGGAGAAACAATAAACTCATTTTCAAAGTGAA
TTTGTTAGAAATGGATGATAAAATATTGGTTGACTTCCGGCTTTCTAAGGGTGATGGATT
GGAGTTCAAGAGACACTTCTGAAGATTAAAGGGAAGCTGATTGATATTGTGAGCAGCCA
GAAGGTTTGGCTTCCCTGCCACATTCGATCGGACCATCGGCTCTGGGGAATCCTGGTGAATAT
AGTGCTGCTATGTTGACATTATTCTTCCCTAGAGAAGATTATCCTGTCCTGCAAACCTGCAA
ATAGTAGTTCCCTGAAGTGTTCACTTCCCTGTTTATCCAAACATCTTCCAATTTATTTGT
TTGTTCCGCATACAAATAATACCTATATCTTAATTGTAAGCAAACTTTGGGGAAAGGAT
GAATAGAATTCATTTGATTATTTCTTCATGTGTGTTTAGTATCTGAATTTGAACTCATC
TGGTGGAAACCAAGTTTCAGGGGACATGAGTTTTCCAGCTTTTATACACACGTATCTCAT
TTTTATCAAAACATTTTGT

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FIGURE 12

MAVPFVEDWDLVQTLGEGAYGEVQLAVNRVTEEAVALVKIVDMKRAVDCPENIKKEICINK
MLNHENVVKFYGHRREGNIQYLFLEYCSGGELFDRIEPDIGMPEPDAQRFFHQLMAGVVY
LHGIGITHRDIKPENLLDERONLKISDFGLATVFRYNNRERLLNKMCGTLPYVAPELLK
RREFHAEPVDVWSCGIVLTAMLAGELPWDQPSDSCQEYSDWKEKKTYLNPWKKIDSAPLA
LLHKILVENPSARITIPDIKKDRWYNKPLKKGAKRPRVTSGGVSESPSGFSKHIQSNLDF
SPVNSASSEENVKYSSSQPEPRTGLSLWDTSPSYIDKLVOGISFSQPTCPDHMLLNSQLL
GTPGSSQNPWQRLVKRMTRFFTKLDADKSYQCLKETCEKLGQWKKSCMNQVTISTDRR
NNKLIFKVNLLLEMDDKILVDFRLSKGDGLEFKRHFLKIKGKLIDIVSSQKVWLPAT

cAMP- and cGMP-dependent protein kinase phosphorylation site.

375-378

Tyrosine kinase phosphorylation site.

383-390

394-402

N-myristoylation site.

123-128

195-200

341-346

361-366

Serine/Threonine protein kinases active-site signature.

126-138

Protein kinase domain

9-265

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FIGURE 13

CCGCGGTTCCGGCTGCTCCGGCGAGGCGACCTTGGGTCGGCGCTGCGGGCGAGGTGGGC
AGGTAGGTGGGCGGACGGCCGCGGTTCTCCGGCAAGCGCAGGCGGGGAGTCCCCACGG
CGCCCGAAGCGCCCCCGCACCCCCGGCTCCAGCGTTGAGGCGGGGGAGTGAGGAGATG
CCGACCCAGAGGGACAGCAGCACCATGTCACACCGGTCGCAGGCGGGCGGCAGCGGGGAC
CATTCCCACCAAGGTCCGGGTGAAAGCCTACTACCGCGGGGATATCATGATAACACATTTT
GAACCTTCCATCTCCTTTGAGGGCCTTTGCAATGAGGTTGAGACATGTGTTCTTTGAC
AACGAACAGCTCTTCACCATGAAATGGATAGATGAGGAAGGAGACCCGTGTACAGTATCA
TCTCAGTTGGAGTTAGAAGAAGCCTTAGACTTTATGAGCTAAACAAGGATTCTGAACCTC
TTGATTCATGTGTCCCTTGTGTACCAGAACGTCTTGGGATGCCTTGTCCAGGAGAAGAT
AAATCCATCTACCGTAGAGGTGCACGCCGCTGGAGAAAAGCTTTATTGTGCCAATGGCCAC
ACTTTCCAAGCCAAGCGTTTCAACAGCGCTGCTCACTGTGCCATCTGCACAGACCGAATA
TGGGGACTTGGACGCCAAGGATATAAGTGCATCAACTGCAAACTCTTGGTTCATAAGAAG
TGCCATAAACTCGTCACAAATTGAATGTGGGCGGCATTCTTTGCCACAGGAACCAAGTGATG
CCCATGGATCAGTCATCCATGCATTCTGACCATGCACAGACAGTAATTCATATAATCCT
TCAAGTCATGAGAGTTTGGATCAAGTTGGTGAAGAAAAAGAGGCAATGAACACCAAGGAA
AGTGGCAAAGCTTCATCCAGTCTAGGTCTTCAGGATTTTGATTGTCTCCGGGTAATAGGA
AGAGGAAGTTATGCCAAAGTACTGTTGGTTCGATTAAAAAAAACAGATCGTATTTATGCA
ATGAAAGTTGTGAAAAAAGAGCTTGTAAATGATGATGAGGATATTGATTGGGTACAGACA
GAGAAGCATGTGTTTGAGCAGGCATCCAATCATCCTTTCCTTGTGGGCTGCATTCTTGC
TTTCAGACAGAAAGCAGATTGTTCTTTGTTATAGAGTATGTAAATGGAGGAGACCTAATG
TTTCATATGCAGCGACAAAGAAAACCTTCTGAAGAACATGCCAGATTTTACTCTGCAGAA
ATCAGTCTAGCATTAATTTATCTTCATGAGCGAGGGATAATTTATAGAGATTTGAAACTG
GACAATGTATTACTGGACTCTGAAGGCCACATTAACTCACTGACTACGGCATGTGTAAG
GAAGGATTACGGCCAGGAGATACAACCAGCACTTTCTGTGGTACTCCTAATTACATTGCT
CCTGAAATTTTAAGAGGAGAAGATTATGGTTTCAGTGTTGACTGGTGGGCTCTTGGAGTG
CTCATGTTTGAGATGATGGCAGGAAGGTCTCCATTTGATATTGTTGGGAGCTCCGATAAC
CCTGACCAGAACACAGAGGATTATCTCTTCCAAGTTATTTTGGAAAAACAAATTCGCATA
CCACGTTCTCTGTCTGTAAAGCTGCAAGTGTTCTGAAGAGTTTCTTAATAAGGACCCCT
AAGGAACGATTGGGTGTCATCTCAACAGGATTTGCTGATATTCAGGGACACCCGTTT
TTCCGAAATGTTGATTGGGATATGATGGAGCAAAAACAGGTGGTACCTCCCTTTAAACCA
AATATTTCTGGGAATTTGGTTTGGACAACCTTTGATTCTCAGTTTACTAATGAACCTGTC
CAGCTCACTCCAGATGACGATGACATTGTGAGGAAGATTGATCAGTCTGAATTTGAAGGT
TTTGAGTATATCAATCCTCTTTTGATGTCTGCAGAAGAATGTGTCTGATCCTCATTTTTC
AACCATGTATTCTACTCATGTTGCCATTTAATGCATGGATAAACTTGCTGCAAGCCTGGA
TACAATTAACCATTTTATATTTGCCACCTACAAAAAACACCCAATATCTTCTCTGTAG
ACTATATGAATCAATTATACATCTGTTTTACTATGAAAAAAAATTAATACTACTAGCT
TCCAGACAATCATGTCAAAATTTAGTTGAACTGGTTTTTCAGTTTTTAAAGGCCTACAG
ATGAGTAATGAAGTTACCTTTTTTGTTTAAAAAAAAG

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FIGURE 14

MSHTVAGGGSGDHSQVRVKAYYRGDIMITHFEPSISFEGLCNEVRDMCSFDNEQLFTMK
WIDEEGDPCTVSSQLELEEEAFRLYELNKDSELLIHVFPCVPERPGMPCPGEDKSIYRRGA
RRWRKLYCANGHTFQAKRFNRRAHCAICTDRIWGLGRQGYKCINCKLLVHKKCHKLV
TIE CGRHSLPQEPVMPMDQSSMHS DHAQTVIPYNPSSHESLDQVGEEKEAMNTRESGKASSSL
GLQDFDLLRVIGRGSYAKVLLVRLKKTDRYAMKVVKELVNDDDEDIDWVQTEKHVFEQA
SNHPFLVGLHSCFQTESRLFFVIEYVNGGDLMFHMQRQRKLPEEHARFYSAEISLALNYL
HERGIIYRDLKLDNVLLDSEGHKLT DYGMCKEGLRPGDTTSTFCGTPNYIAPEILRGED
YGFSDWWALGVLMFEMMAGRSPFDIVGSSDNDPDQNTEDYLEFQVILEKQIRIPRSLSVKA
ASVLKSFLNKDPKERLGCHPQTGFADIQGHPPFRNVWDMMEQKQVVPFPKPNISGEFGL
DNFDSQFTNEPVQLTPDDDDIVRKIDQSEFEGFEYINPLLMSAEECV

N-glycosylation site.

533-536

Tyrosine kinase phosphorylation site.

265-271

N-myristoylation site.

7-12
308-313
394-399

Cell attachment sequence.

24-26

Serine/Threonine protein kinases active-site signature.

365-377

Protein kinase domain
245-513

Protein kinase C terminal domain
514-580

Phorbol esters/diacylglycerol binding domain
132-181

Octicosapeptide repeat
56-85

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FIGURE 15

GGGGCGGGCGGGCGCAGTTTGCTCATACTTTGTGACTTGCGGTACAGTGGCATTTCAGC
TCCACACTTGGTAGAACACAGGCACGACAAGCATAGAAACATCCTAAACAATCTTCATC
GAGGCATCGAGGTCCATCCCAATAAAAATCAGGAGACCCTGGCTATCATAGACCTTAGTC
TTCGCTGGTATACTCGCTGTCTGTCAACCAGCGGTTGACTTTTTTTAAGCCTTCTTTTTT
CTCTTTTACAGTTTCTGGAGCAAATTCAGTTTGCCTTCCTGGATTTGTAAATTGTAATG
ACCTCAAACTTTAGCAGTTCTTCCATCTGACTCAGGTTTGCTTCTCTGGCGGTCTTCAG
AATCAACATCCACACTTCCGTGATTATCTGCGTGCATTTTGGACAAAGCTTCCAACCAGG
ATACGGGAAGAAGAAATGGCTGGTGATCTTTCAGCAGGTTTCTTCATGGAGGAACCTTAAT
ACATACCGTCAGAAGCAGGGAGTAGTACTTAAATATCAAGAAGTGCCTAATTCAGGACCT
CCACATGATAGGAGGTTTACATTTCAAGTTATAATAGATGGAAGAGAATTTCCAGAAGGT
GAAGGTAGATCAAAGAAGGAAGCAAAAAATGCCGCAGCCAAATTAGCTGTTGAGATACTT
AATAAGGAAAAGAAGGCAGTTAGTCCTTTATTATTGACAACAACGAATTCCTCAGAAGGA
TTATCCATGGGGAATTACATAGGCCTTATCAATAGAATTGCCCAGAAGAAAAGACTAACT
GTAATTTATGAACAGTGTGCATCGGGGGTGCATGGGCCAGAAGGATTTCAATTATAAATGC
AAAATGGGACAGAAAAGAAATATAGTATTGGTACAGGTTCTACTAAACAGGAAGCAAAACAA
TTGGCCGCTAAACTTGCATATCTTCAGATATTATCAGAAGAAACCTCAGTGAAATCTGAC
TACCTGTCTCTGGTCTTTTTGCTACTACGTGTGAGTCCCAAAGCAACTCTTTAGTGACC
AGCACACTCGCTTCTGAATCATCATCTGAAGGTGACTTCTCAGCAGATACATCAGAGATA
AATTTCTAACAGTGACAGTTTAAACAGTTCTTCGTTGCTTATGAATGGTCTCAGAAATAAT
CAAAGGAAGGCAAAAGATCTTTGGCACCCAGATTTGACCTTCCTGACATGAAAGAAACA
AAGTATACTGTGGACAAGAGGTTTGGCATGGATTTTAAAGAAATAGAATTAATTGGCTCA
GGTGGATTTGGCCAGTTTTCAAAGCAAAACACAGAATTGACGGAAAGACTTACGTTATT
AAACGTGTTAAATATAATAACGAGAAGGCGGAGCGTGAAGTAAAAGCATTGGCAAAACTT
GATCATGTAATATTGTTCACTACAATGGCTGTTGGGATGGATTTGATTATGATCCTGAG
ACCAGTGATGATTCTCTTGAGAGCAGTGATTATGATCCTGAGAACAGCAAAAATAGTTCA
AGGTCAAAGACTAAGTGCTTTTTCATCCAAATGGAATTCCTGTGATAAAGGGACCTTGGAA
CAATGGATTGAAAAAAGAAGAGGCGAGAAACTAGACAAAGTTTGGCTTTGGAACCTCTT
GAACAAATAACAAAAGGGGTGGATTATATACATTCAAAAAATTAATTCATAGAGATCTT
AAGCCAAAGTAATATATTCTTAGTAGATACAAAACAAGTAAAGATTGGAGACTTTGGACTT
GTAACATCTCTGAAAAATGATGGAAAGCGAACAAAGGAGTAAGGGAACCTTGGCATACATG
AGCCCAAGACAGATTTCTTCGCAAGACTATGGAAAGGAAGTGGACCTCTACGCTTTGGGG
CTAATTTCTGTGAACTTCTTCATGTATGTGACACTGCTTTTGAAACATCAAAGTTTTTC
ACAGACCTACGGGATGGCATCATCTCAGATATATTTGATAAAAAAGAAAAAATCTTCTA
CAGAAATTACTCTCAAAGAAAACCTGAGGATCGACCTAACACATCTGAAATACTAAGGACC
TTGACTGTGTGGAAGAAAAGCCCAGAGAAAAATGAACGACACACATGTTAGAGCCCTTCT
GAAAAAGTATCCTGCTTCTGATATGCAGTTTTCCTTAAATTATCTAAAATCTGCTAGGGA
ATATCAATAGATATTTACCTTTTTATTTAATGTTTCCTTTAATTTTTTACTATTTTACT
AATCTTTCTGCAGAAACAGAAAGGTTTTCTTCTTTTTTGTCTTCAAAAACATTCTTACATTT
TACTTTTTCTGGCTCATCTCTTTATTCTTTTTTTTTTTTTTAAAGACAGAGTCTCGCTC
TGTTGCCAGGCTGGAGTGCAATGACACAGTCTTGGCTCACTGCAACTTCTGCTCTTGG
GTTCAAGTGATTCTCCTGCCTCAGCCTCCTGAGTAGCTGGATTACAGGCATGTGCCACCC
ACCCAATAATTTTTGTGTTTTTAATAAAGACAGGGTTTTACCATGTTGGCCAGGCTGGT
CTCAAACCTCCTGACCTCAAGTAATCCACCTGCCTCGGCCTCCCAAAGTGCTGGGATTACA
GGGATGAGCCACCGCGCCAGCCTCATCTCTTTGTTCTAAAGATGGAAAAACCCGCCA
AATTTTCTTTTTTATACTATTAATGAATCAATCAATTCATATCTATTTATTAAATTTCTAC
CGCTTTTAGGCCAAAAAATGTAAGATCGTTCTCTGCCTCACATAGCTTACAAGCCAGCT
GGAGAAATATGGTACTCATTAAAAAAGTGAATGTACAACC

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FIGURE 16

MAGDLSAGFFMEELNTYRQKQGVLKYQELPNSGPPHRRFTFQVIIDGREFPEGEGRSK
KEAKNAAAKLAVEILNKEKKAVSPLLLTTTNSSEGLSMGNYIGLINRIAQKKRLTVNYEQ
CASGVHGPGEFHYKCKMGQKEYSIGTGSTKQEAQQLAAKLAYLQILSEETSVKSDYLSSG
SFATTCESQSNLVTSTLASESSSEGDFSADTSEINSNSDSLNSSSLLMNGLRNNQRKAK
RSLAPRFDLPDMKETKYTVDKRFGMDFKIEELIGSGGFGQVFKAKHRIDGKTYVIKRVKY
NNEKAEREVKALAKLDHVNIVHYNGCWDGFDYDPETSDDSLESSDYDPENSKNSSRSKTK
CLFIQMEFCDKGTLEQWIEKRRGEKLDKVLALFLFEQITKGVDYIHSKKLIHRDLKPSNI
FLVDTKQVKIGDFGLVTSKNDGKRTRSKGTLRYMSPEQISSQDYGKEVDLYALGLILAE
LLHVCDTAFETSKFFTDLRDGIISDIFDKKEKTLQKLLSKKPEDRPNTSEILRTLTVWK
KSPEKNERHTC

N-glycosylation site.

91-94
223-226
353-356
528-531

cAMP- and cGMP-dependent protein kinase phosphorylation site.

39-42
112-115

Tyrosine kinase phosphorylation site.

285-293

N-myristoylation site.

95-100
99-104
145-150
180-185
231-236
325-330
434-439
475-480

Amidation site.

442-445

Serine/Threonine protein kinases active-site signature.

410-422

Protein kinase domain

267-538

Double-stranded RNA binding motif

10-75
101-165

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FIGURE 17

ATGTCTCGGGAGTCGGATGTTGAGGCTCAGCAGTCTCATGGCAGCAGTGCCTGTTACACAG
CCCCATGGCAGCGTTACCCAGTCCCAAGGCTCCTCCTCACAGTCCCAGGGCATATCCAGC
TCCTCTACCAGCACGATGCCAACTCCAGCCAGTCCTCTCACTCCAGCTCTGGGACACTG
AGCTCCTTAGAGACAGTGTCCACTCAGGAACCTCTATTCTATTCTGAGGACCAAGAACCT
GAGGACCAAGAACCTGAGGAGCCTACCCCTGCCCCCTGGGCTCGATTATGGGCCCTTCAG
GATGGATTTGCCAATCTTGAATGTGTGAATGACAACACTACTGGTTTGGGAGGGACAAAAGC
TGTGAATATTGCTTTGATGAACCACTGCTGAAAAGAACAGATAAAATACCGAACATACAGC
AAGAAACACTTTTCGGATTTTCAGGGAAGTGGGTCTAAAACTCTTACATTGCATACATA
GAAGATCACAGTGGCAATGGAACCTTTGTAAATACAGAGCTTGTAGGGAAAGGAAAACGC
CGTCCTTTGAATAACAATTCTGAAATTGCACTGTCACTAAGCAGAAATAAAGTTTTTGTC
TTTTTTGATCTGACTGTAGATGATCAGTCAGTTTATCCTAAGGCATTAAGAGATGAATAC
ATCATGTCAAAAACCTCTTGGAAGTGGTGCCTGTGGAGAGGTAAAGCTGGCTTTTCGAGAGG
AAAACATGTAAGAAAGTAGCCATAAAGATCATCAGCAAAAGGAAGTTTGCTATTGGTTCA
GCAAGAGAGGCAGACCCAGCTCTCAATGTTGAAACAGAAATAGAAATTTTGAAAAAGCTA
AATCATCCTTGCATCATCAAGATTAAAACTTTTTTTGATGCAGAAGATTATTATATTGTT
TTGGAATTGATGGAAGGGGGAGAGCTGTTTGACAAAGTGGTGGGGAATAAACGCCTGAAA
GAAGCTACCTGCAAGCTCTATTTTTACCAGATGCTCTTGGCTGTGCAGTACCTTCATGAA
AACGGTATTATACACCGTGACTTAAAGCCAGAGAATGTTTTACTGTCTCATCTCAAGAAGAG
GACTGTCTTATAAAGATTACTGATTTTGGGCACTCCAAGATTTTGGGAGAGACCTCTCTC
ATGAGAACCTTATGTGGAACCCCCACCTACTTGGCGCCTGAAGTTCTTGTTTCTGTTGGG
ACTGCTGGGTATAACCGTGCTGTGGACTGCTGGAGTTTAGGAGTTATTCTTTTTATCTGC
CTTAGTGGGTATCCACCTTTCTCTGAGCATAGGACTCAAGTGTCACTGAAGGATCAGATC
ACCAGTGGAAAATACAACCTTCATTCCCTGAAGTCTGGGCAGAAGTCTCAGAGAAAGCTCTG
GACCTTGTCAGAAGTTGTTGGTAGTGGATCCAAAGGCACGTTTTACGACAGAAGAAGCC
TTAAGACACCCGTGGCTTCAGGATGAAGACATGAAGAGAAAGTTTCAAGATCTTCTGTCT
GAGGAAAATGAATCCACAGCTCTACCCCAGGTTCTAGCCCAGCCTTCTACTAGTCGAAAG
CGGCCCCGTGAAGGGGAAGCCGAGGGTGCCGAGACCACAAAGCGCCAGCTGTGTGTGCT
GCTGTGTTGTGAACTCCGTGGTTTGAACACGAAAGAAATGTCCTTCTTTCACTCTGCATC
TTTCTTTTCTTTGAGTCGTTTTTTTATAGTTGGATTTAATTATGGAATAATGGTTT

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FIGURE 18

MSRES DVEAQQSHGSSACSQPHGSVTQSQGSSSSQSQGISSSSSTSTMPNSSQSSHSSSGTL
SSLETVSTQELYSIPE DQEPEDQEP EPTPAPWARLWALQDGFANLECVNDNYWFG RDKS
CEYCFDEPLLKRTDKYRTYSKKHFRI FREVGPKN SYIAYIEDHSGNGTFVNTELVGKGKR
RPLNNNSEIALSLSRNKVFVFFDLTVDDQSVYPKALRDEYIMSKTLGSGACGEVKLA FER
KTCKKVAIKIISKRKFAIGSAREADPALNVETEIEILKKLNHP CIIKIKNFFDAEDYYIV
LELMEGGELFDKVVGNKRLKEATCKLYFYQMLLAVQYLHENGIIHRDLKPENVLLSSQEE
DCLIKITDFGH SKILGETSLMRTL CGTPTYLAPEVLVSVGTAGYNRAVDCWSLGVILFIC
LSGYPPFSEHRTQVSLKDQITSGKYNFIPEVWAEVSEKALDLVKKLLVVDPKARFTTEEA
LRHPWLQDEDMKRKFQDLLSEENESTALPQVLAQPSTSRKRPREGEAEGAETTKRPAVCA
AVL

N-glycosylation site.

48-51
166-169
185-188
503-506

Glycosaminoglycan attachment site.

164-167

Tyrosine kinase phosphorylation site.

289-297

N-myristoylation site.

14-19
37-42
58-63
167-172
227-232
529-534

Amidation site.

177-180

Serine/Threonine protein kinases active-site signature.

343-355

Protein kinase domain

220-486

FHA domain

113-192

22/46

FIGURE 19

GGCACGAGTAGGGGTGGCGGGTCAGTGTCTCGGGGGCTTCTCCATCCAGGTCCCTGGA
GTTCTTGGTCCCTGGAGCTCCGCACTTGGCGCGCAACCTGCGTGAGGCAGCGGACTCTG
GCGACTGGCCGGCCATGCTTCCCGGGCTGAGGACTATGAAGTGTTGTACACCATTTGGCA
CAGGCTCCTACGGCCGCTGCCAGAAGATCCGGAGGAAGAGTGATGGCAAGATATTAGTTT
GGAAAGAACTTGACTATGGCTCCATGACAGAAGCTGAGAAACAGATGCTTGTCTGAAG
TGAATTTGCTTCGTGAACGAAACATCCAAACATCGTTCGTTACTATGATCGGATTATTG
ACCGGACCAATACAACACTGTACATTGTAATGGAATATTGTGAAGGAGGGGATCTGGCTA
GTGTAATTACAAAGGGAACCAAGGAAAGGCAATACTTAGATGAAGAGTTTGTCTTCGAG
TGATGACTCAGTTGACTCTGGCCCTGAAGGAATGCCACAGACGAAGTGATGGTGGTCATA
CCGTATTGCATCGGGATCTTAAACCAGCCAATGTTTTCTGGATGGCAAGCAAAACGTCA
AGCTTGGAGACTTTGGGCTAGCTAGAATATTAAACCATGACACGAGTTTTGCAAAAACAT
TTGTTGGCACACCTTATTACATGTCTCCTGAACAAATGAATCGCATGTCTACAATGAGA
AATCAGATATCTGGTCATTGGGCTGCTTGTGTATGAGTTATGTGCATTAATGCCTCCAT
TTACAGCTTTTAGCCAGAAAGAACTCGCTGGGAAAATCAGAGAAGGCAAATTCAGGCGAA
TTCCATACCGTTACTCTGATGAATTGAATGAAATTATTACGAGGATGTTAACTTAAAGG
ATTACCATCGACCTTCTGTTGAAGAAATTCTTGAGAACCCTTTAATAGCAGATTTGGTTG
CAGACGAGCAAAGAAGAAATCTTGAGAGAAGAGGGCGACAATTAGGAGAGCCAGAAAAAT
CGCAGGATTCCAGCCCTGTATTGAGTGAGCTGAACTGAAGGAAATTCAGTTACAGGAGC
GAGAGCGAGCTCTCAAAGCAAGAGAAGAAAGATTGGAGCAGAAAGAACAGGAGCTTTGTG
TTCGTGAGAGACTAGCAGAGGACAACTGGCTAGAGCAGAAAAATCTGTTGAAGAATACTA
GCTTGCTAAAGGAACGGAAGTTCTGTCTCTGGCAAGTAATCCAGAACTTCTTAATCTTC
CATCCTCAGTAATTAAGAAGAAAGTTCAATTTAGTGAGGGGAAAGTAAAGAGAACATCATGA
GGAGTGAGAATTCTGAGAGTCAGCTCACATCTAAGTCCAAGTGCAAGGACCTGAAGAAAA
GGCTTCACGCTGCCAGCTGCGGGCTCAAGCCCTGTGAGATATTGAGAAAAATTACCAAC
TGAAAGCAGACAGATCCTGGGCATGCGCTAGCCAGGTAGAGAGACACAGAGCTGTGTAC
AGGATGTAATATTACCAACCTTTAAAGACTGATATTCAAATGCTGTAGTGTTGAATACTT
GGCCCCATGAGCCATGCCTTTCTGTATAGTACACATGATATTTCCGAATTGGTTTTACTG
TTCTTCAGCAACTATTGTACAAAATGTTACATTTAATTTTTCTTTCTTTTAAAGAAC
ATATTATAAAAAGAATACTTTCTTGGTTGGGCTTTTAACTCTGTGTGTGATTACTAGTAG
GAACATGAGATGTGACATTCTAAATCTTGGGAGAAAAATAATATTAGGAAAAAAATATT
TATGCAGGAAGAGTAGCACTCACTGAATAGTTTTAAATGACTGAGTGGTATGCTTACAAT
TGTCATGTCTAGATTTAAATTTTAAAGTCTGAGATTTTAAATGTTTTTGAGCTTAGAAAAC
CCAGTTAGATGCAATTTGGTCATTAATACCATGACATCTTGCTTATAAATATTCCATTGC
TCTGTAGTTCAAATCTGTTAGCTTTGTGAAAATTCATCACTGTGATGTTTGTATTCTTTT
TTTTTTCTGTTTAAACAGAATATGAGCTGTCTGTCATTTACCTACTTCTTTCCACTAAA
TAAAAGAATTCCTTCAGTTA

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FIGURE 20

MPSRAEDYEVLYTIGTGSYGRCQKIRRKSDGKILVWKELDYGSMTEAEKQMLVSEVNLLR
ELKHPNIVRYDRIIDRTNTTLYIVMEYCEGGDLASVITKGTKERQYLDEEFVLRVMTQL
TLALKECHRRSDGGHTVLHRDLKPANVFLDGKQNVKLGDFGLARILNHDTSFAKTFVGTP
YYMSPEQMNRMSSYNEKSDIWSLGCCLLYELCALMPPTAFSQQELAGKIREGKFERRIPYRY
SDELNEIITRMLNLKDYHRPSVEEILENPLIADLVADEQRRNLERRGRQLGEPEKSQDSS
PVLSELKLKEIQLERERALKAREERLEQKEQELCVRRERLAEDKLARAENLLKNYSLLKE
RKFLSLASNPELLNLPSSVIKKKVHFSGESKENIMRSENSESQLTSSKCKDLKKRLHAA
QLRAQALS DIEKNYQLKSRQILGMR

N-glycosylation site.

79-82
354-357

cAMP- and cGMP-dependent protein kinase phosphorylation site.

26-29

Tyrosine kinase phosphorylation site.

100-107

N-myristoylation site.

91-96

Leucine zipper pattern.

306-327
313-334

Serine/Threonine protein kinases active-site signature.

137-149

Protein kinase domain

8-271

24/46

FIGURE 21

TTGGCGGGCGGAAGCGGCCACAACCCGGCGATCGAAAAGATTCTTAGGAACGCCGTACCA
GCCGCGTCTCTCAGGACAGCAGGCCCTGTCTTCTGTGCGGGCGCCGCTCAGCCGTGCC
TCCGCCCTCAGGTTCTTTTTCTAATTCCAATAAACTTGCAAGAGGACTATGAAAAGATT
ATGATGAACTTCTCAAATATTATGAATTACATGAACTATTGGGACAGGTGGCTTTGCAA
AGGTCAAACCTTGCTGCCATATCCTTACTGGAGAGATGGTAGCTATAAAAAATCATGGATA
AAAACACACTAGGGAGTGATTTGCCCCGGATCAAAACGGAGATTGAGGCCTTGAAGAACC
TGAGACATCAGCATATATGTCAACTCTACCATGTGCTAGAGACAGCCAACAAAATATTCA
TGGTTCTTGAGTACTGCCCTGGAGGAGAGCTGTTTACTATATAATTTCCAGGATCGCC
TGTCAGAAGAGGAGACCCGGGTGTCTTCCGTCAGATAGTATCTGCTGTTGCTTATGTGC
ACAGCCAGGGCTATGCTCACAGGGACCTCAAGCCAGAAAATTTGCTGTTTGATGAATATC
ATAAATTAAGCTGATTGACTTTGGTCTCTGTGCAAAACCCAAGGGTAACAAGGATTACC
ATCTACAGACATGCTGTGGGAGTCTGGCTTATGCAGCACCTGAGTTAATACAAGGCAAAT
CATATCTTGGATCAGAGGCAGATGTTTGGAGCATGGGCATACTGTTATATGTTCTTATGT
GTGGATTTCTACCATTTGATGATGATAATGTAATGGCTTTATAACAAGAAGATTATGAGAG
GAAAATATGATGTTCCCAAGTGGCTCTCTCCAGTAGCATTCTGCTTCTTCAACAAATGC
TGCAGGTGGACCCAAAGAAACGGATTTCTATGAAAATCTATTGAACCATCCCTGGATCA
TGCAAGATTACAACATATCCTGTTGAGTGGCAAAGCAAGAATCCTTTTATTCACCTCGATG
ATGATTGCGTAACAGAACCTTTCTGTACATCACAGAAACAACAGGCAAACAATGGAGGATT
TAATTTCACTGTGGCAGTATGATCACCTCACGGCTACCTATCTTCTGCTTCTAGCCAAGA
AGGCTCGGGGAAAACCAAGTTCGTTTAAGGCTTTCTTCTTTCTCCTGTGGACAAGCCAGTG
CTACCCCATTCACAGACATCAAGTCAAATAATTGGAGTCTGGAAGATGTGACCGCAAGTG
ATAAAAATTATGTGGCGGGATTAATAGACTATGATTGGTGTGAAGATGATTTATCAACAG
GTGCTGCTACTCCCCGAACATCACAGTTTACCAAGTACTGGACAGAATCAAATGGGGTGG
AATCTAAATCATTAACTCCAGCCTTATGCAGAACACCTGCAAATAAATTAAAGAACAAG
AAAATGTATATACTCCTAAGTCTGCTGTAAAGAATGAAGAGTACTTTATGTTTCTTGAGC
CAAAGACTCCAGTTAATAAGAACCAGCATAAGAGAGAAATACTCACTACGCCAAATCGTT
ACACTACACCCTCAAAGCTAGAAACCAGTGCCTGAAAGAACTCCAATTAATAATACCAG
TAAATTCAACAGGAACAGACAAGTTAATGACAGGTGTCATTAGCCCTGAGAGGCGGTGCC
GCTCAGTGGAATTGGATCTCAACCAAGCACATATGGAGGAGACTCCAAAAAGAAAGGGAG
CCAAAGTGTGTTGGGAGCCTTGAAAGGGGGTTGGATAAGGTTATCACTGTGCTCACCAGGA
GCAAAAGGAAGGGTTCTGCCAGAGACGGGCCAGAAAGACTAAAGCTTCACTATAATGTGA
CTACAAC TAGATTAGTGAATCCAGATCAACTGTTGAATGAAATAATGTCTATTCTTCCAA
AGAAGCATGTTGACTTTGTACAAAAGGGTTATACACTGAAGTGTCAAACACAGTCAGATT
TTGGGAAAGTGACAATGCAATTTGAATTAGAAGTGTGCCAGCTTCAAAAACCCGATGTGG
TGGGTATCAGGAGGCAGCGGCTTAAGGGCGATGCCTGGGTTTACAAAAGATTAGTGGAAG
ACATCCTATCTAGCTGCAAGGTATTAATTGATGGATTCTTCCATCCTGCCGGATGAGTGTG
GGTGTGATACAGCCTACATAAAGACTGTTATGATCGCTTTGATTTTAAAGTTCATTGGAA
CTACCAACTTGTGTTCTAAAGAGCTATCTTAAGACCAATATCTCTTTGTTTTTAAACAAA
GATATTATTTGTGTATGAATCAATCAAGCCCATCTGTCATTATGTTACTGTCTTTTT
TAATCATGTGGTTTTGTATATTAATAATTGTTGACTTCTTAGATTCACTTCCATATGTG
AATGTAAGCTCTTAACATATGTCTCTTTGTAATGTGTAATTTCTTTCTGAAATAAACCAT
TTGTGAATAT

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FIGURE 22

MKDYDELLKYYELHETIGTGGFACVVKLACHILTGEMVAIKIMDKNTLGSDLPRIKTEIEA
LKNLRHQHICQLYHVLETANKIFMVLEYCPGGELFDYIISQDRLSEEETRVVFRQIVSAV
AYVHSQGYAHRDLKPENLLFDEYHKLKLDIFGLCAKPKGNKDYLQTCCGSLAYAAPELI
QGKSYLGSEADVWSMGILLYVLMCGFLPFDDDDNVMALYKKIMRGKYDVPKWLSPPSSILL
QQMLQVDPKKRISMKNLLNHPWIMQDYNYPVEWQSKNPFHLDODDCVTELSVHHRNNROT
MEDLISLWQYDHLTATYLLLLAKKARGKPVRLRLSSSFSCGQASATPFTDIKSNNWSLEDV
TASDKNYVAGLIDYDWCEDDLSTGAATPRTSQFTKYWTESNGVESKSLTPALC RTPANKL
KNKENVYTPKSAVKNEEYFMFPEPKTPVNKNQHKREILTPNRYTTPSKARNQCLKETPI
KIPVNSTGTDKLMTGVISPERRCRSVELDLNQAHEETPKRKGAKVFGSLERGLDKVITV
LTRSKRKGSARDGPRLKLHYNVTTRLVNPQQLNEIMSLPKKHVDFVQKGYTLKCQT
QSDFGKVTMQFELEVCQLQKPDVVGI RRQLKGDWVYKRLVEDILSSCKV

N-glycosylation site.

354-357
485-488
562-565

cAMP- and cGMP-dependent protein kinase phosphorylation site.

250-253
546-549

Tyrosine kinase phosphorylation site.

2-10
421-427
630-638

N-myristoylation site.

340-345

Microbodies C-terminal targeting signal.

649-652

Leucine zipper pattern.

165-186

Serine/Threonine protein kinases active-site signature.

128-140

Protein kinase domain

11-263

Kinase associated domain 1

602-651

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FIGURE 23

GTCTTTATTTTCAGTCCCGGATCCGCGGGCGCAGGCCAGCTCAGGCCCCAGGGATGGAC
GTCGTGGACCTGACATTTTCAATAGAGACCCCGGGACCCTATGACCTGCTACAGCGG
CTGGGTGGCGGCACGTATGGGGAAGTCTTTAAGGCTCGAGACAAGGTGTCAGGGGACCTG
GTGGCACTGAAGATGGTGAAGATGGAGCCTGATGATGATGTCTCCACCCTTCAGAAGGAA
ATCCTCATATTGAAAACCTTGCCGGCACGCCAACATCGTGGCCTACCATGGGAGTTATCTC
TGGTTGCAGAACTCTGGATCTGCATGGAATTCTGTGGGGCTGGTTCTCTCCAGGACATC
TACCAAGTGACAGGCTCCCTGTCAGAGCTCCAGATTAGCTATGTCTGCCGGGAAGTGCTC
CAGGGACTGGCCTATTTGCACTCACAGAAGAAGATACACAGGGACATCAAGGGAGCTAAC
ATCCTCATCAATGATGCTGGGGAGGTGAGATTGGCTGACTTTGGCATCTCGGCCAGATT
GGGGCTACACTGGCCAGACGCCTCTCTTTCATTGGGACACCCTACTGGATGGCTCCGGAA
GTGGCAGCTGTGGCCCTGAAGGGAGGATACAATGAGCTGTGTGACATCTGGTCCCTGGGC
ATCACGCCATCGAACTGGCCGAGCTACAGCCACCGCTCTTTGATGTGCACCCTCTCAGA
GTTCTCTTCTCATGACCAAGAGTGGCTACCAGCCTCCCCGACTGAAGGAAAAAGGCAAA
TGGTCGGCTGCCTTCCACAACCTTCATCAAAGTCACTCTGACTAAGAGTCCCAAGAAACGA
CCCAGCGCCACCAAGATGCTCAGTCATCAACTGGTATCCCAGCCTGGGCTGAATCGAGGC
CTGATCCTGGATCTTCTTGACAACTGAAGAATCCCGGGAAAGGACCCTCCATTGGGGAC
ATTGAGGATGAGGAGCCCGAGCTACCCCCCTGCTATCCCTCGGCGGATCAGATCCACCCAC
CGCTCCAGCTCTCTGGGGATCCCAGATGCAGACTGCTGTGCGGCGGCACATGGAGTTCAGG
AAGCTCCGAGGAATGGAGACCAGACCCCGAGCCAACACCGCTCGCCTACAGCCTCCTCGA
GACCTCAGGAGCAGCAGCCCCAGGAAGCAACTGTGAGAGTCGTCTGACGATGACTATGAC
GACGTGGACATCCCCACCCCTGCAGAGGACACACCTCCTCCACTTCCCCCAAGCCCAAG
TTCCGTTCTCCATCAGACGAGGGTCTGAGGAGCATGGGGGATGATGGGCAGCTGAGCCCG
GGGGTGCTGGTCCGGTGTGCCAGTGGGCCCCCACCAACAGCCCCCGTCTGGGGCTCCC
CCATCCACAGCAGCCCCACCTCACCGCCCATTCAGAACCTCACTCTGGAACCCACCC
TCCCGGGAGCTTGACAAGCCCCACTTCTGCCCCCAAGAAGGAAAAGATGAAGAGAAAAG
GGATGTGCCCTTCTCGTAAAGTTGTTCAATGGCTGCCCCCTCCGGATCCACAGCACGGCC
GCCTGGACACATCCCTCCACCAAGGACCAGCACCTGCTCCTGGGGGAGAGGAAGGCATC
TTCATCCTGAACCGAATGACCAGGAGGCCACGCTGGAAATGCTCTTTCTAGCCGGACT
ACGTGGGTGTACTCCATCAACAACGTTCTCATGTCTCTCTCAGGAAAGACCCCCACCTG
TATTCTCATAGCATCCTTGGCCTGCTGGAACGGAAGAGACCAGAGCAGGAAACCCCATC
GCTCACATTAGCCCCCACCCTACTGGCAAGGAAGAACATGGTTTCCACCAAGATCCAG
GACACCAAGGCTGCCGGGCGTGCTGTGTGGCGGAGGGTGCAGGCTCTGGGGGCCCGTTC
CTGTGCGGTGCATTGGAGACGTCCGTTGTCTGCTTTCAGTGGTACCAGCCCATGAACAAA
TTCCTGCTTGTCCGGCAGGTGCTGTTCCCACTGCCGACGCCTCTGTCCGTGTTTCGCGCTG
CTGACCGGGCCAGGCTCTGAGCTGCCCGCTGTGTGCATCGGCGTGAGCCCCGGGCGGCCG
GGGAAGTCGGTGCTCTTCCACACGGTGCGCTTTGGCGCGCTCTCTTGCTGGCTGGGCGAG
ATGAGCACCGAGCACAGGGGACCCGTGCAGGTGACCCAGGTAGAGGAAGATATGGTGATG
GTGTTGATGGATGGCTCTGTGAAGCTGGTGACCCCGAGGGGTCCCCAGTCCGGGGACTT
CGCACACCTGAGATCCCCATGACCGAAGCGGTGGAGGCCGTGGCTATGGTTGGAGGTGAG
CTTCAGGCCTTCTGGAAGCATGGAGTGCAGGTGTGGGCTCTAGGCTCGGATCAGCTGCTA
CAGGAGCTGAGAGACCTACCTTCACTTTCCGTCTGCTTGGCTCCCCCAGGCTGGAGTGC
AGTGGCACGATCTCGCCTCACTGCAACCTCCTCCTCCAGGTTCAAGCAATTCTCCTGCC
TCAGCCTCCCGAGTAGCTGGGATTACAGGCCCTGAGTGGTGGAGACACGCCAGTGGATG
ATCCTACTGCTCCAGCAACCTCTACATCCAGGAATGAGTCCCTAGGGGGGTGTGAGGAA
CTAGTCCTTGACCCCCCTCCCCATAGACACACTAGTGGTCATGGCATGTCTCATCTCC
CAATAAACATGACTTTAGCCTCTGCAAAAAAA

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FIGURE 24

MDVVDPDIFNRDPRDHYDLLQRLGGGTYGEVFKARDKVSGLVALKMKMEPDDDDVSTLQ
KEILILKTCRANIVAYHGSYLWLQKLWICMEFCGAGSLQDIYQVTGSLSELQISYVCRE
VLQGLAYLHSQKKIHRDIKANILINDAGEVRLADFGISAQIGATLARRLSFIGTPYWMA
PEVAVALKGGYNELCDIWSLGITAIELAELOPPLFDVHPLRVLFMTKSGYQPPRLKEK
GKWSAAFHNFIKVTLTSPKKRPSATKMLSHQLVSPGLNRGLILDLLDKLKNPGKGPSI
GDIEDEEPPELPPAIRRIRSTHRSSSLGIPDADCCRRHMEFRKL RGMETRPPANTARLQP
PRDLRSSSPRKQLSESSDDDDYDDVDIPTPAEDTPPPLPPKPKFRSPSDEGPGSMGDDGQL
SPGVLVRCASGPPPNSPRPGPPPSTSSPHLTAHSEPSLWNPPSRELDKPPLPPKKEKMK
RKGCALLVKLFNGCPLRIHSTAATHPSTKDQHLLLGAEGLFILNRNDQEATLEMLFPS
RTTWVYSINNVLMSLSGKTPHLYSHSILGLLERKETRAGNPPIAHISPHRLLARKNMVSTK
IQDTKGCRAACVAEGASSGGPFLCGALETSSVLLQWYQPMNKFLLRQVLFPLPTPLSVF
ALLTGPGSELPAVCIGVSPGRPGKSVLFHTVRFALSCWL GEMSTEHRGPVQVTQVEEDM
VMVLMGDSVKLVTPEGSPVRGLRTPPEIPMTEAVEAVAMVGGQLQAFWKHGVQVWALGSDQ
LLQELRDPPTLTFRLLGSPRLECSGTISPHCNLLLPSSNSPASASRVAGITGL

cAMP- and cGMP-dependent protein kinase phosphorylation site.

168-171
261-264
573-576

N-myristoylation site.

25-30
163-168
278-283
328-333
517-522
579-584
606-611
615-620
625-630
676-681
694-699
761-766

CNH domain
500-805

Protein kinase domain

17-274

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FIGURE 25

GAATTCGGCACGAAGGAGAGTAGCAGTGCCTTGGACCCCAGCTCTCCTCCCCCTTTCTCT
CTAAGGATGGCCCCAGAAGGAGAACTCCTACCCCTGGCCCTACGGCCGACAGACGGCTCCA
TCTGGCCTGAGCACCTGCCCCAGCGAGTCTCCGGAAAGAGCCTGTCACCCCATCTGCA
CTTGTCCTCATGAGCCGCTCCAATGTCCAGCCCACAGCTGCCCCCTGGCCAGAAGGTGATG
GAGAATAGCAGTGGGACACCCGACATCTTAACGCGGCACTTCACAATTGATGACTTTGAG
ATTGGGCGTCTCTGGGCAAAGGCAAGTTTGGAAACGTGTACTTGGCTCGGGAGAAGAAA
AGCCATTTTCATCGTGGCGCTCAAGGTCCTCTTCAAGTCCCAGATAGAGAAGGAGGGCGTG
GAGCATCAGCTGCGCAGAGAGATCGAAATCCAGGCCACCTGCACCATCCCAACATCCTG
CGTCTCTACAACATATTTTTATGACCGGAGGAGGATCTACTTGATTCTAGAGTATGCCCC
CGCGGGGAGCTCTACAAGGAGCTGCAGAAGAGCTGCACATTTGACGAGCAGCGAACAGCC
ACGATCATGGAGGAGTTGGCAGATGCTCTAATGTACTGCCATGGGAAGAAGGTGATTCAC
AGAGACATAAAGCCAGAAAATCTGCTCTTAGGGCTCAAGGGAGAGCTGAAGATTGCTGAC
TTCGGCTGGTCTGTCCATGCGACCTCCCTGAGGAGGAAGACAATGTGTGGCACCCTGGAC
TACCTGCCCCCAGAGATGATTGAGGGGCGCATCGACAATGAGAAGGTGGATCTGTGGTGC
ATTGGAGTGCTTTTGCTATGAGCTGCTGGTGGGGAACCCATTTGAGAGTGCATCACACAAC
GAGACCTATCGCCGCATCGTCAAGGTGGACCTAAAGTTCCCGCTTCTGTGCCCCACGGGA
GCCCAGGACCTCATCTCCAACTGCTCAGGCATAACCCCTCGGAACGGCTGCCCCTGGCC
CAGGTCTCAGCCCACCTTGGGTCCGGGCCAACTCTCGGAGGGTGCTGCCTCCCTCTGCC
CTTCAATCTGTGCGCTGATGGTCCCTGTCATTCACTCGGGTGCGTGTGTTTGTATGTCTG
TGTATGTATAGGGGAAAGAAGGGATCC

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FIGURE 26

MAQKENSYPWPYGRQTAPSGLSTLPQRVLRKEPVTPSALVLMSRSNVQPTAAPGQKVMEN
SSGTPDILTRHFTIDDFEIGRPLGKGKFGNVYLAREKKSHFIVALKVLFKSQIEKEGVEH
QLRREIEIQAHLHHPNILRLYNFYDRRIYLLILEYAPRGELYKELQKSCTFDEQRTATI
MEELADALMYCHGKKVIHRDIKPENLLLGLKGELKIADFGWSVHATSLRRKTMCGTLDYL
PPEMIEGRIDNEKVDLWCIGVLCYELLVGNPFESASHNETYRRIVKVDLKFPASVPTGAQ
DLISKLLRHNPSERLPLAQVSAHPWVRANSRRVLPPSALQSV

N-glycosylation site.

60-63
278-281

cAMP- and cGMP-dependent protein kinase phosphorylation site.

229-232

Amidation site.

192-195

Serine/Threonine protein kinases active-site signature.

196-208

Protein kinase domain

77-326

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FIGURE 27A

GGAATTCCTTTTTTTTTTTTTTTTTTGGAGATGGAGTTTCACTCTTGTGGCCAGGCTGGAGTG
CAATGGCACAATCTCAGCTTACTGCAACCTCCGCCCTCCCGGGTTCAGCGATTCTCCTGC
CTCAGCCTCTCAAGTAGCTGGGATTACAGGCATGTGCCACCACCCCTGGCTAACTAATTT
CTTTTCTATTTAGTAGAGATGGGGTTTACCCTGTTGGTCAGGCTGGTCTTGAACCTCTG
ACCTCAGGTGATCCACTTGCCTTGGCCTCCCAAAGTGCTAGGATTACAGCCGTGAAACTG
TGCCTGGCTGATTCTTTTTTTTGTGTTGGATTTTGAACAGGGTCTCCCTTGGTCGCCC
AGGCTGGAGTGCAGTGGTGCATCTTGGCTCACTATAACCTCCACCTCCTGGTTTTCAAGT
GATCCTCCCACCTTAGCCTCCTGAGTAGCTGTGATTACAGGCGTGACCACCACACCCGG
CTAATTTTTGTATTTTTATTAGAGACAGGGTTTACCCTGTTGGCCAGGCTGTTCTCAAA
CTCCTGGACTCAAGGGATCCGCCTGCCTCCACTTCCCAAAGTCCCGAGATTACAGGTGTG
AGTCACCATGCCTGACCTTATAATTTCTTAAGTCATTTTTTCTGGTCCATTTCTTCCCTTAG
GGTCCCTCACAACAAATCTGCATTAGGCGGTACAATAATCCTTAACCTTCATGATTCACAAA
AGGAAGATGAAGTGATTCATGATTTAGAAAGGGGAAGTAGTAAGCCCACTGCACACTCCT
GGATGATGATCCTAAATCCAGATACAGTAAAAATGGGGTATGGGAAGGTAGAATACAAAA
TTTGGTTTTAAATTAATTATCTAAATATCTAAAAACATTTTTGGATACATTGTTGATGTGA
ATGTAAGACTGTACAGACTTCTAGAAAACAGTTTGGGTTCATCTTTTTCATTTCCCCAG
TGCAGTTTTCTGTAGAAATGGAATCCGAGGATTTAAGTGGCAGAGAATTGACAATTGATT
CCATAATGAACAAAGTGAGAGACATTAAAAATAAGTTTAAAAATGAAGACCTTACTGATG
AACTAAGCTTGAATAAAATTTCTGCTGATACTACAGATAACTCGGGAACGTGTTAACCAAA
TTATGATGATGGCAAACAACCCAGAGGACTGGTTGAGTTTGTGCTCAAACCTAGAGAAAA
ACAGTGTTCGGCTAAGTGATGCTCTTTTAAATAAATTGATTGGTCGTTACAGTCAAGCAA
TTGAAGCGCTTCCCCAGATAAATATGGCCAAAATGAGAGTTTTGCTAGAAATTCAGTGA
GATTTGCTGAATTAAGGCTATTCAAGAGCCAGATGATGCACGTGACTACTTTCAAATGG
CCAGAGCAAACCTGCAAGAAATTTGCTTTTGTTCATATATCTTTTGCACAATTTGAACGTG
CACAAGGTAATGTCAAAAAAGTAAACAACCTTCTTCAAAAAGCTGTAGAACGTGGAGCAG
TACCACTAGAAATGCTGGAAATTTGCCCTGCGGAATTTAAACCTCCAAAAAAGCAGCTGC
TTTCAGAGGAGGAAAAAGAAGATTTATCAGCATCTACGGTATTAACCTGCCCAAGAAATCAT
TTTCCGGTTCACTTGGGCATTTACAGAAATAGGAACAACAGTTGTGATTCCAGAGGACAGA
CTACTAAAGCCAGGTTTTTATATGGAGAGAACATGCCACCACAAGATGCAGAAATAGGTT
ACCGGAATTCATTGAGACAAACTAACAAAACCTAAACAGTCATGCCCATTTGGAAGAGTCC
CAGTTAACCTTCTAAATAGCCAGATTGTGATGTGAAGACAGATGATTCAGTTGTACCTT
GTTTTATGAAAAGACAAACCTCTAGATCAGAATGCCGAGATTTGGTTGTGCTGGATCTA
AACCAAGTGGAAATGATTCCTGTGAATTAAGAAATTTAAAGTCTGTTCAAAATAGTCATT
TCAAGGAACCTCTGGTGTGATGAAAAGAGTTCTGAACCTATTATTACTGATTCAATAA
CCCTGAAGAATAAAACGGAATCAAGTCTTCTAGCTAAATTAGAAGAACTAAAGAGTATC
AAGAACCAGAGGTTCCAGAGAGTAACCAGAAACAGTGGCAAGCTAAGAGAAAGTCAGAGT
GTATTAACCAGAATCCTGCTGCATCTTCAATCACTGGCAGATTCCGGAGTTAGCCCGAA
AAGTTAATACAGAGCAGAAACATACCACCTTTTGAGCAACCTGTCTTTTCAGTTTCAAAAC
AGTCACCACCAATATCAACATCTAAATGGTTTGACCCAAAATCTATTTGTAAGACACCAA
GCAGCAATACCTTGGATGATTACATGAGCTGTTTTAGAAGTCCAGTTGTAAGAATGACT
TTCCACCTGCTTGTGTCAGTTGTCAACACCTTATGGCCAACCTGCCTGTTTCCAGCAGCAAC
AGCATCAATACTTGGCACTCCACTTCAAAATTTACAGGTTTTAGCATCTTCTTCAGCAA
ATGAATGCATTTTCGGTTAAAGGAAGATTTATTCATATTAAGCAGATAGGAAGTGGAG
GTTCAAGCAAGGTATTTTCAGGTGTTAAATGAAAAGAAACAGATATATGCTATAAAATATG
TGAACCTAGAAGAAGCAGATAACCAAACTCTTGATAGTTACCGGAACGAAATAGCTTATT
TGAATAAACTACAACAACACAGTGATAAGATCATCCGACTTTATGATTATGAAATCACGG
ACCAGTACATCTACATGGTAATGGAGTGTGGAAATATTGATCTTAATAGTTGGCTTAAAA
AGAAAAATCCATTGATCCATGGGAACGCAAGAGTTACTGGAAAAATATGTTAGAGGCAG
TTCACACAATCCATCAACATGGCATTGTTACAGTGATCTTAAACCAGCTAACTTTCTGA
TAGTTGATGGAATGCTAAAGCTAATTGATTTTGGGATTGCAAACCAATGCAACCAGATA
CAACAAGTGTGTTAAAGATTCTCAGGTGGGCACAGTTAATTATATGCCACCAGAAGCAA
TCAAAGATATGTCTTCTCCAGAGAGAAATGGGAAATCTAAGTCAAAGATAAGCCCCAAAA
GTGATGTTTGGTCTTAGGATGTATTTGTACTATATGACTTACGGGAAAAACACCATTTT
AGCAGATAATTAATCAGATTTCTAAATTACATGCCATAATTGATCCTAATCATGAAATTG
AATTTCCCGATATTCCAGAGAAAGATCTTCAAGATGTGTTAAAGTGTGTTTAAAAAGGG
ACCCAAAACAGAGGATATCCATTCTGAGCTCCTGGCTCATCCATATGTTCAAATTCAAA
CTCATCCAGTTAACCAATGGCCAAGGGAACCACTGAAGAAATGAAATATGTTCTGGGCC
AACTTGTGGTCTGAATTTCTCCTAACTCCATTTTGAAAGCTGCTAAAACCTTATATGAAC
ACTATAGTGGTGGTGAAAGTCATAATCTTTCATCCTCCAAGACTTTTGAAAAAAAAGGG
GAAAAAAATGATTTGCAGTTATTCGTAATGTGATAGGAGGTATAAAATATATTGGACT
GTTATACTCTTGAATCCCTGTGGAATCTACATTTGAAGACAACATCACTCTGAAGTGT
ATCAGCAAAAAAATTCAGTGAGATTATCTTTAAAGAAAACGTGAAAAATAGCAACCAC

FIGURE 27A

TTATGGCACTGTATATATTGTAGACTTGTTTTCTCTGTTTTATGCTCTTGTGTAATCTAC
TTGACATCATTTTACTCTTGGAATAGTGGGTGGATAGCAAGTATATTCTAAAAAAGTTTG
TAAATAAAGTTTTGTGGCTAAATGA

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FIGURE 28

MNKVRDIKNKFKNEDLTDELSLNKISADTTDNSGTVNQIMMMANNPEDWLSLLLKLEKNS
VPLSDALLNKLIGRYSQAIEALPPDKYQNESFARIQVRFAELKAIQEPDDARDYFQMAR
ANCKKFAFVHISFAQFELSQGNVKKSKQLLQKAVERGAVPLEMLEIALRNLNLQKKQLLS
EEEKKNLSASTVLTAQESFSGSLGHLQNRNNSCDSRGQTTKARFLYGENMPPQDAEIGYR
NSLRQTNKTKQSCPPFGRVPVNLNLPDCDVKTDDSVVPCFMKRQTSRSECRDLVVPGSKP
SGNDSCELRNLKSVQNSHFKEPLVSDEKSSELIITDSITLKNKTESSLLAKLEETKEYQE
PEVPESNQKQWQAKRKSECINQNPAASSNHWQIPELARKVNTEQKHTTTEQPVFSVSKQS
PPISTSKWFDPKSICKTPSSNTLDDYMSCFRTPVVKNDFPPACQLSTPYGQPACFQQQQH
QILATPLQNLQVLASSSANECISVKGRIYSILKQIGSGGSSKVFLNEKKQIYAIKYVN
LEEADNQTLDSYRNEIAYLNKLQQHSDKIIRLYDYEITDQYIYVMECGNIDLNSWLKKK
KSIDPWERKSYWKNMLEAVHTIHQHGIVHSDLKPANFLIVDGMKLIDFGIANQMOPDTT
SVVKDSQVGTVNYMPPEAIKDMSSSRENGKSKSKISPKSDVWSLGCILYYMTYGKTPFQQ
IINQISKLHAIIDPNHEIEFPDIPEKDLQDVLKCLKRDPKQRISIPELLAHPYVQIQTH
PVNQMAKGTTEEMKYVLGQLVGLNSPNSILKAAKTLYEHYSGGESHNSSSSKTFEKKRGK
K

N-glycosylation site.

90-93
186-189
210-213
247-250
303-306
342-345
546-549
827-830

cAMP- and cGMP-dependent protein kinase phosphorylation site.

282-285
374-377
599-602

Tyrosine kinase phosphorylation site.

351-358
787-796

N-myristoylation site.

88-93
297-302
302-307
470-475
516-521
626-631
798-803

Amidation site.

838-841

Serine/Threonine protein kinases active-site signature.

627-639

Protein kinase domain

509-775

FIGURE 29

GAATTCGCGGCCGCGTTCGACGATCTCTTGGAGACGGCGACCCAGGCATCTGGGGAGCCAC
AGAAGTCGTACTCCCTTAAACCCTGCTTTGGCTCCCCCTGTGGATGTAACCCCTTAGCTGG
CATTTTGCATCTCAATTGGCTTGTGATGGAGGCGTCTTTGGGGATTAGATGGATGAGCC
AATGGCTTTTTCTCCCCAGCGTGACCGGTTTCAGGCTGAAGGCTCTTTAAAAAAAACGA
GCAGAATTTTAACTTGCAGGTGTTAAAAAAGATATTGAGAAGCTTTATGAAGCTGTACC
ACAGCTTAGTAATGTGTTTAAAGATTGAGGACAAAATTGGAGAAGGCACTTTCAGCTCTGT
TTATTTGGCCACAGCACAGTTACAAGTAGGACCTGAAGAGAAAATTGCTCTAAACACTT
GATTTCCAACAAGTCATCCTATAAGAATTGCAGCTGAACCTTCAGTGCCTAACAGTGGCTGG
GGGGCAAGATAATGTCATGGGAGTTAAATACTGCTTTAGGAAGAATGATCATGTAGTTAT
TGCTATGCCATATCTGGAGCATGAGTCGTTTTTGGACATTCTGAATTCTCTTTCCTTTCA
AGAAGTACGGGAATATATGCTTAATCTGTTCAAAGCTTTGAAACGCATTCATCAGTTTGG
TATTGTTACCGTGATGTTAAGCCCAGCAATTTTTTATATAATAGGCGCCTGAAAAAGTA
TGCCTTGGTAGACTTTGGTTTGGCCCAAGGAACCCATGATACGAAAATAGAGCTTCTTAA
ATTTGTCCAGTCTGAAGCTCAGCAGGAAAGGTGTTCAAAAACAAATCCACATAATCAC
AGGAAACAAGATTCCACTGAGTGGCCAGTACCTAAGGAGCTGGATCAGCAGTCCACCAC
AAAAGCTTCTGTTAAAAGACCTACACAAATGCACAAATTCAGATTAAACAAGGAAAAGA
CGGAAAGGAGGGATCTGTAGGCCCTTCTGTCCAGCGCTCTGTTTTTGGAGAAAAGAAATTT
CAATATACACAGCTCCATTTTACATGAGAGCCCTGCAGTGAACCTCATGAAGCAGTCAAA
GACTGTGGATGTACTGTCTAGAAAGTTAGCAACAAAAAGAAGGCTATTTCTACGAAAGT
TATGAATAGTGTCTGTGATGAGGAAAAGTCCAGTTCTTGGCCAGCTAGCCTGACCTGTGA
CTGCTATGCAACAGATAAAGTTTGTAGTATTTGCTTTTCAAGGCGTCAGCAGGTTGCCCC
TAGGGCAGGTACACCAGGATTCAGAGCACCAGAGGTCTTGACAAAGTGCCCCAATCAAAC
TACAGCAATTGACATGTGGTCTGCAGGTGTCATATTTCTTTTCTTGTAGTGGACGATA
TCCATTTTATAAAGCAAGTGATGATTTAACTGCTTTGGCCCAAATTTATGACAATTAGGGG
ATCCAGAGAACTATCCAAGCTGCTAAAACCTTTGGGAAATCAATATTATGTAGCAAAGA
AGTTCAGCACAAGACTTGAGAAAACCTCTGTGAGAGACTCAGGGGTATGGATTCTAGCAC
TCCAAGTTAAACAAGTGATATACAAGGGCATGCTTCTCATCAACCAGCTATTTCAAGAA
GACTGACCATAAAGCTTCTGCTCGTTCAAACACCTCCAGGACAATACTCAGGGAATTC
ATTTAAAAAGGGGGATAGTAATAGCTGTGAGCATTGTTTTGATGAGTATAATACCAATTT
AGAAGGCTGGAATGAGGTACCTGATGAAGCTTATGACCTGCTTGATAAACTTCTAGATCT
AAATCCAGCTTCAAGAATAACAGCAGAAGAAGCTTTGTTGCATCCATTTTTTAAAGATAT
GAGCTTGTGATAATGGATCTTCATTTAATGTTTACTGTTATGAGGTAGAATAAAAAAGAA
TACTTTGTAAATAGCCACAAGTTCTTGTTTAGAGACCAGAGCAGGATTAATAATTTATTTT
AACATTTTAGTGTGTTGGTGGCACATTCTAAAATATAGATTAAAGAATACTTAAAAATGCCTG
GGATAGTTCTTGGGACTAACACATGATCTTCTTTGAGTTAAACCTACCTAAGTAGATTT
TAGGTGGGTTCTTATAGGTGAGATTTTATAGCTTCCCTAATTACCTTTCACTGACATACA
GAAAAAGGAGCAGTTTTAGTTTTAATTAATTAATAAATAACAGATGTGATGAGGATTAAAT
GAATCAAAAAGACTTAATTTGTAGATTCTTTTAGAGTTATGAGCTAGGTATAGTTTGGGGA
AACTCAACCTGGTGTGCTGCTTAAACAATTTTGTAATAAAGAAGATAATTTCTCTTTT
CTAGAGGTACATATTAGGCCTTTTATGAACACTAAAACAATGAGGAAATGTTGGTCATGG
GGCAAAGTATCACTTAAAAATTGAATTCATCCATTTTTTAAAAACACTTCATGAAAGCATT
CTGGTGTGAATTGCCATTTTTTCTTACTGGCTTCTCAATTTTCTTCTCTCTGCCCCCT
ACCTAAAACATTCTCCTCGGAAATTACATGGTGCTGACCACAAAGTTTCTGGATGTTTTA
TTAAATATTGTACGTGTTTACAGTTGGGAATTTAAATAATACATACACTGGTTGATAAA
GGGAAGCTGCAGGACCAAGGTGAAGATTGATAGTCCAAATGCTTTTCTTTTTTGTAGTTGT
ATATTTTTTACACCATCTTAGATATAATTAGGTAGCTGCTGAAAGGAAAAGTGAATACA
GAATTGACGGTATTATTGGAGATTTTTCTCTGCGTAGAGCCATCCAGATCTCTGTATCC
TGTTTTGACTAAGTCTTAGGTGGGTTGGGAAGACAGATAATGAAGTAGGCAAAGAGAAAA
GGACCAAGATAGAGGTTTATATTAGAAATGGTATATATCAATGACAGCATATCAAACCT
TCCTATGGGAAAAAGTCTGGTGGGTGGTCAGCTGACAGATTTCCCATTTAGTAGTCATAG
AATACAGAAATAGTTTAGGGACATGTATTCATTTTTGTTATTTTTGAGCATTGATAGGTCAG
TATATCTACCTAATCTGTTTGGTAAGTATAGGATATATAAACCATTACCATTGATCTGTC
TTATGCCATAATCTTAAAAAAAATGAATGCTCTTGAATTTGTATATTCAATAAAGTTA
TCCTTTTATAAAAAAAAAGTCGACGCGGCCGC

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FIGURE 30

MEASLGIQMDEPMAFSPQRDRFOAEGSLKKNEQNFKLAGVKKDIEKLYEAVPQLSNVFKI
EDKIGEGTFSSVYLATAQLQVGPEEKIALKHLIPTSHPIRIAAELQCLTVAGGQDNVMGV
KYCFRKNHDHVVIAMPYLEHESFLDILNSLSFQEVREYMLNLFKALKRIHQFGIVHRDVKP
SNFLYNRRLKKYALVDFGLAQGTHDTKIELLKFFVQSEAQQERCSQNKSHIITGNKIPLSG
PVPKELDQQSTTKASVKRPYTNAQIQIKQKGKDGKEGSLVQSVFGERNFNIHSSISH
ESPAVKLMKQSKTVDVLSRKLATKKKAISTKVMNSAVMRKTASSCPASLTCDYATDKVC
SICLSRRQOVAPRAGTPGFRAPEVLTKCPNQTTAIDMWSAGVIFLSLLSGRYPFYKASDD
LTALAQIMTIRGSRETIQAAKTFGKSILCSKEVPAQDLRKLKERLRGMDSSSTPKLTSDIQ
GHASHQPAISEKTDHKASCLVQTPPGQYSGNSFKKGDSNSCEHCFDEYNTNLEGWNEVPD
EAYDLLDKLLDLNPASRITAEALLHPFFKDMSL

N-glycosylation site.

226-229
390-393

Tyrosine kinase phosphorylation site.

41-48

N-myristoylation site.

67-72
112-117
119-124
198-203
202-207
432-437
467-472
506-511

ATP/GTP-binding site motif A (P-loop).

439-446

Serine/Threonine protein kinases active-site signature.

173-185

Protein kinase domain

58-569

35/46

FIGURE 31

CCGAGTTACGAGTCGGCGAAAGCGGGCGGGAAGTTCGTACTGGGCAGAACGCGACGGGTCT
GCGGCTTAGGTGAAAATGCCTCGTGTAAGCAGCTCAAGCTGGAAGACAGAGCTCTGCA
AAGAGACATCTTGCAGAACAATTTGCAGTTGGAGAGATAATAACTGACATGGCAAAAAAG
GAATGGAAAGTAGGATTACCCATTGGCCAAGGAGGCTTTGGCTGTATATATCTTGCTGAT
ATGAATTCCTCAGAGTCAGTTGGCAGTGATGCACCTTGTGTTGTAAAAGTGGAAACCCAGT
GACAATGGACCTCTTTTTACTGAATTAAAGTTCTACCAACGAGCTGCAAAACCAGAGCAA
ATTCAGAAATGGATTTCGTACCCGTAAGCTGAAGTACCTGGGTGTTCCTAAGTATTGGGGG
TCTGGTCTACATGACAAAAATGGAAAAAGTTACAGGTTTATGATAATGGATCGCTTTGGG
AGTGACCTTCAGAAAATATATGAAGCAAATGCCAAAAGGTTTTCTCGGAAAACGTCTTG
CAGCTAAGCTTAAGAATTCTGGATATTCTGGAATATATTCACGAGCATGAGTATGTGCAT
GGAGATATCAAGGCCCTCAAATCTTCTTCTGAAC TACAAGAATCCTGACCAGGTGTACTTG
GTAGATTATGGCCTTGCTTATCGGTACTGCCCAGAAGGAGTTCATAAAGAATACAAAGAA
GACCCCAAAGATGTCACGATGGCACTATTGAATTCACGAGCATCGATGCACACAATGGT
GTGGCCCCATCAAGACGTGGTGATTTGGAAATACCTTGTTATTGCATGATCCAATGGCTT
ACTGGCCATCTTCTTGGGAGGATAATTTGAAAGATCCTAAATATGTTAGAGATTCCAAA
ATTAGATACAGAGAAAATATTGCAAGTTTGATGGACAAATGTTTCTCTGAGAAAAACAAA
CCAGGTGAAATTGCCAAATACATGGAAACAGTGAAATTACTAGACTACACTGAAAAACCT
CTTTATGAAAATTTACGTGACATTCTTTTGCAAGGACTAAAAGCTATAGGAAGTAAGGAT
GATGGCAAATTTGGACCTCAGTGTTGTGGAGAATGGAGGTTTGAAAGCAAAAAACAATAACA
AAGAAGCGAAAGAAAGAAATTGAAGAAAGCAAGGAACCTGGTGTTGAAGATACGGAATGG
TCAAACACACAGACAGAGGAGGCCATACAGACCCGTTCAAGAACCAGAAAGAGAGTCCAG
AAGTAATTCAGATGCTGTGAACCAGATTTCTTTCTTTGTTTTCTTTTGACTTTTTTCT
CCTTTTCTGTTAGAACTGTTTTATTTTCTGTGAGTCTTGCGAGGTGGAATTAATGATTA
AATACTCATGTGTTTCAAGAAACATAAACTTTTTTTATAAAAAATATTTTGTACAATTCATT
AAAGGCTAATTTATGAAATTTGAAATCTTCAGGTTATACTCCTTAAGTTATCCCAAAGC
CGTGTGTTTGTGATGTTTTGGAGTACATATATATGAAAATTATTATGACACGCACTTTTC
TAATCATTGTACATTTCTCAGAGTGGATAAAAAATGTTTGACAAAGTCCTCACTTTTAAGG
AAATGCAAAGCTTAAAAATAAACTCTTTTTGTTTGTATGCAG

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FIGURE 32

MPRVKAAQAGRQSSAKRHLAEQFAVGEIITDMAKKEWKVGLPIGQGGFGCIYLADMNSSE
SVGSDAPCVVKVEPSDNGPLFTELKFYQRAAKPEQIQKWIRTRKLKYLGVPKYWGSGLHD
KNGKSYRFMIMDRFGSDLQKIYEANAKRFSRKTVLQLSLRILDILEYIHEHEYVHGDIKA
SNLLLNKPNPDQVYLVLDYGLAYRYCPEGVHKEYKEDPKRCHDGTIEFTSIDAHNGVAPSR
RGDLEILGYCMIQWLTGHLPWEDNLKDPKYVRDSKIRYRENIASLMDKCFPEKNKPGEIA
KYMETVKLLDYTEKPLYENLRDILLQGLKAIGSKDDGKLDLSVVENGGLKAKTITKKRKK
EIEESKEPGVEDTEWSNTQTEEAIQTRSRTKRKRVQK

N-glycosylation site.

57-60

cAMP- and cGMP-dependent protein kinase phosphorylation site.

147-150

Tyrosine kinase phosphorylation site.

160-167

188-194

241-249

295-302

N-myristoylation site.

40-45

46-51

235-240

347-352

369-374

Cell attachment sequence.

241-243

Serine/Threonine protein kinases active-site signature.

173-185

Protein kinase domain

37-325

FIGURE 33

AGTTGGCGGGAATGGCTGCTCGCGGAGGGGCGAGTGACGCGGGGCGCTGTAGGCTGTCC
AGCGATGGATCCACCGCGGGAAGCAAGAAGGAGCCTGGAGGAGGCGCGGCGACTGAGGA
GGGCGTGAATAGGATCGCAGTGCCAAAGCCGCCCTCCATTGAGGAATTCAGCATAGTGAA
GCCCATTAGCCGGGCGCCTTCGGGAAAGTGTATCTGGGGCAGAAAGGCGGCAAATTGTA
TGCAGTAAAGGTTGTTAAAAAGCAGACATGATCAACAAAAATATGACTCATCAGGTCCA
AGCTGAGAGAGATGCACTGGCACTAAGCAAAAGCCCATTTCATTGTCCATTTGTATTATTC
ACTGCAGTCTGCAACAATGTCTACTTGGTAATGGAATATCTTATTGGGGGAGATGTCAA
GTCTCTCCTACATATATATGGTTATTTTGTATGAAGAGATGGCTGTGAAATATATTTCTGA
AGTAGCACTGGCTCTAGACTACCTTCACAGACATGGAATCATCCACAGGGACTTGAAACC
GGACAATATGCTTATTTCTAATGAGGGTCATATTAACTGACGGATTTTGGCCTTTCAAA
AGTTACTTTGAATAGAGATATTAATATGATGGATATCCTTACAACACCATCAATGGCAAA
ACCTAGACAAGATTATTCAAGAACCCAGGACAAGTGTTATCGCTTATCAGCTCGTTGGG
ATTTAACACACCAATTGCAGAAAAAATCAAGACCCTGCAACATCCTTTAGCCTGTCT
GTCTGAAACATCAGCCTTTCTCAAGGACTCGTATGCCCTATGTCTGTAGATCAAAAGGA
CACTACGCCTTATTCTAGCAAATTACTAAAATCATGTCTTGAAACAGTTGCCTCCAACCC
AGGAATGCCTGTGAAGTGTCTAACTTCTAATTTACTCCAGTCTAGGAAAAGGCTGGCCAC
ATCCAGTGCCAGTAGTCAATCCACACCTTCATATCCAGTGTGGAATCAGAATGCCACAG
CAGTCCCAAATGGGAAAAAGATTGCCAGGAAAGTGATGAAGCATTGGGCCCCAACAATGAT
GAGTTGGAATGCAGTTGAAAAGTTATGCGCAAAATCTGCAAATGCCATTGAGACGAAAGG
TTTCAATAAAAAGGATCTGGAGTTAGCTCTTTCTCCATTTCATAACAGCAGTGCCCTTCC
CACCCTGGACGCTCTTGTGTAAACCTTGCTAAAAAATGCTTCTCTGGGGAAGTTTCTTG
GGAAGCAGTAGAAGTGGATGTAAATAATATAAATATGGACACTGACACAAGTCAGTTAGG
TTTCCATCAGTCAAATCAGTGGGCTGTGGATTCTGGTGGGATATCTGAAGAGCACCTTGG
GAAAAGAAAGTTAAAAAGAAATTTGAGTTGGTTGACTCCAGTCTTGTAAAAAATTAT
ACAGAATAAAAAAATCTGTAGAGTATAAGCATAACGAAATGACAAATTGTTATACAAA
TCAAAATACAGGCTTAACAGTTGAAGTGCAGGACCTTAAGCTATCAGTGCACAAAAGTCA
ACAAAATGACTGTGCTAATAAGGAGAACATTGTCAATTCCTTTACTGATAAACAACAAAC
ACCAGAAAAATTACCTATACCAATGATAGCAAAAAACCTTATGTGTGAAGTTCGATGAAGA
CTGTGAAAAGAAATAGTAAGAGGGACTACTTAAGTTCTAGTTTCTATGTTCTGATGATGA
TAGAGCTTCTAAAAATATTTCTATGAAGTCTGATTCTCTTTCTGGAATTTCTATAAT
GGAAAGTCCATTAGAAAAGTCAGCCCTTAGATTTCAGATAGAAGCATTAAAGAATCCTCTTT
TGAAGAATCAAATATGAAGATCCACTTATTGTAACACCAGATTGCCAAGAAAAGACCTC
ACCAAAGGTGTGAGAAACCTGCTGTACAAGAGAGTAACCAAAAAATGTTAGGTCTCTCC
TTTGGAGGTGCTGAAAACGTTAGCCTCTAAAAGAAATGCTGTTGCTTTTCGAAGTTTAA
CAGTCATATTAATGCATCCAATAACTCAGAACCATCCAGAATGAACATGACTTCTTTAGA
TGCAATGGATATTTTCGCGTGCCTACAGTGGTTCATATCCCATGGCTATAACCCCTACTCA
AAAAAGAGATCCTGTATGCCACATCAGACCCCAATCAGATCAAGTCGGGAAGTCCATA
CCGAAGTCCGAAGAGTGTGAGAAGAGGGGTGGCCCCCGTTGATGATGGGCGAATTCTAGG
AACCCAGACTACCTTGACCTGAGCTGTTACTAGGCAGGGCCCATGGTCTCTGCGGTAGA
CTGGTGGGCACTTGGAGTTTGCTTGTGTTGAATTTCTAACAGGAATTCCTTTCAATGA
TGAAACACCACAACAAGTATTCCAGAATATCTGAAAAGAGATATCCCTTGCCAGAAAGG
TGAAGAAAAGTTATCTGATAATGCTCAAAGTGCAGTAGAAATACTTTTAACCATTGATGA
TACAAAGAGAGCTGGAATGAAAGAGCTAAAACGTCATCTCTCTTCAGTGATGTGGACTG
GGAAAATCTGCAGCATCAGACTATGCCTTTCATCCCCAGCCAGATGATGAAACAGATAC
CTCCTATTTTGAACACAGGAATACTGCTCAGCACCTGACCGTATCTGGATTTAGTCTGTA
GCACAAAAATTTTCTTTTAGTCTAGCCTCGTGTTATAGAATGAAGTTCATAATTATAT
ACTCCTTAATACTAGATTGATCTAAGGGGGAAAGATCATTATTTAACCTAGTTCAATGTG
CTTTTAATGTACGTTACAGCTTTACAGAGTTAAAAGGCTGAAAGGAATATAGTCAGTAA
TTTATCTTAACCTCAAACTGTATATAAATCTTCAAAGCTTTTTCATCTATTTATTTTG
TTTATTGCACTTTATGAAAAGTGAAGCATCAATAAAATTAGAGGACACTATTGAGAGTGA
GCCACTAGCTTGATTTTCTTTCTCTCTGATTTTCAGTTCACTGTTTCAGTTTAGCATTA
ATAATAAAATAATCATACAGTTCC

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FIGURE 34

MDPTAGSKKEPGGGAATEEGVNRIAVPKPPSIEEFSIVKPISRGAFGKVYLGQKGGKLYA
VKVVKKADMINKNMTHQVQAERDALALSKSPFIVHLYYSLQSANNVYLVMEYLIGGDVKS
LLHIYGYFDEEMAVKYI SEVALALDYLHRHGIIHRDLKPDNMLISNEGH IKLTD FGLSKV
TLNRDINMMDILTTSPMAKPRQDYSRTPGQVLSLISSLG FNTPIAEKNQDPANILSACLS
ETSQLSQGLVCPMSVDQKDTTPYSSKLLKSCLETVASNPGMPVKCLTSNLLQSRKRLATS
SASSQSHTFISSVESECHSSPKWEKDCQESDEALGPTMMSWNAVEKLCAKSANAIETKGF
NKKDLELALSPIHNSSALPTTGRSCVNLAKKCFSGEVSWEAVELDVNNINMDTDTSQLGF
HQSNQWAVDSGGISEEHLGKRSLKRN FELVDSSPCKKIIQNKKTCVEYKHNEMTNCYTNO
NTGLTVEVQDLKLSVHKSQQNDCANKENIVNSFTDKQQTPEKLPIPMIAKNLMCELEDC
EKNSKRDYLSSSF L C S D D D R A S K N I S M N S D S S F P G I S I M E S P L E S Q P L D S D R S I K E S S F E
ESNIEDPLIVTPDCQEKTS PKGVENPAVQESNQKMLGPPLEVLKTLASKRNAVAFRSFNS
HINASNNSEPSRMNMTSLDAMDISRAYS GSYPMAITPTQKRRSCMPHQTPNQIKSGTPYR
TPKSVRRGVAPVDDGRILGTPDYLAPELLLGRAHGPAVDWWALGVCLFEFLTGI PPFNDE
TPQQVFQNILKRDI PWPEGEEKLSDNAQSAVEILLTIDTKRAGMKELKRHPLFSDVDWE
NLQHQTMPFIPQPDDETDTSYFETRNTAQHLTVSGFSL

N-glycosylation site.

73-76
374-377
564-567
663-666
666-669
674 -677

cAMP- and cGMP-dependent protein kinase phosphorylation site.

700-703

N-myristoylation site.

12-17
13-18
52-57
209-214

Amidation site.

438-441

Serine/Threonine protein kinases active-site signature.

152-164

Protein kinase domain

35-834

39/46

FIGURE 35

CAAGAGCCCTTCCTGCAGGGAACCTCAGGCTTCAGAGAGCCGAAAAGTTGGGAGGCGTAA
CCACTTACAGGCCGGAAGTGTCGGGGGTGGACGCATTTCGGGTAGCCGAAGAAGTCCCAGG
ATTGCCGAAGAAGTCCCAGGATTTCCGAAGCGAGCCGAAGCATCGCGACAGTTTTTCAGAG
ACAGCTGATCGGTTGGAGCTGTTGCGCCGAGCAGTCATGGCGGCGGCCAGAGCTACTACG
CCGGCCGATGGCGAGGAGCCCCGCCCGGAGGCTGAGGCTCTGGCCGCAGCCCCGGGAACGG
AGCAGCCGCTTCTTGAGCGGCCTGGAGCTGGTGAAGCAGGGTGCCGAGGCGCGCTGTTT
CGTGGCCGCTTCCAGGGCCGCGCGGCGGTGATCAAGCACCGCTTCCCCAAGGGCTACCGG
CACCCGCGCTGGAGGCGCGGCTTGGCAGACGGCGGACGGTGACAGGAGGCCCGGGCGCTC
CTCCGCTGTCGCGCGCTGGAATATCTGCCCCAGTTGTCTTTTTTGTGGACTATGCTTCC
AACTGCTTATATATGGAAGAAATTGAAGGCTCAGTGAAGTTCGAGATTATATTCAGTCC
ACTATGGAGACTGAAAAAACTCCCCAGGGTCTCTCCAAGTACCAAGACAATTGGGCAG
GTTTTGGCTCGAATGCACGATGAAGACCTCATTGATGATCTCACCACCTCCAACATG
CTCCTGAAACCCCCCTGGAACAGCTGAACATTGTGCTCATAGACTTTGGGCTGAGTTTT
ATTTAGCACTTCCAGAGGATAAGGGAGTAGACCTCTATGTCCTGGAGAAGGCCTTCCTC
AGTACCCATCCCAACACTGAACTGTGTTTGAAGCCTTTCTGAAGAGCTACTCCACCTCC
TCCAAAAGGCCAGGCCAGTGCTAAAAAAATTAGATGAAGTGCGCCTGAGAGGAAGAAAG
AGGTCCATGGTTGGGTAGAAGAATGTGTATGACAACACACACAGTGAAGCTCTTTTTTC
AAAGTAAATTTGAAGAAATGCTACAAGTATGAGATGAGATCTAAGTAAAGGTGTTAAGAT
ATTAAAAA

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FIGURE 36

MAAARATTPADGEEPAPEAEALAAARERSRFLSGLELVKQGAEARVFRGRFQGRAAVIK
HRFPKGYRHPALEARLGRRRTVQEARALLRCRRAGISAPVVFVVDYASNCLYMEEIEGSV
TVRDYIQSTMETEKTPOGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLEQLNIV
LIDFGLSFISALPEDKGVDLYVLEKAFLSTHPNTETVFEAFLKSYSTSSKKARPVLKKLD
EVRLRGRKRSMVG

cAMP- and cGMP-dependent protein kinase phosphorylation site.

78-81
247-250

N-myristoylation site.

147-152

Amidation site.

76-79
245-248

Tyrosine protein kinases specific active-site signature.

158-170

Protein kinase domain

33-252

41/46

FIGURE 37

AGCGCGCGACTTTTTGAAAGCCAGGAGGGTTCGAATTGCAACGGCAGCTGCCGGGCGTAT
GTGTTGGTGCTAGAGGCAGCTGCAGGGTCTCGCTGGGGGCCGCTCGGGACCAATTTTGAA
GAGGTACTTGGCCACGACTTATTTTCACCTCCGACCTTTCCTTCCAGGCGGTGAGACTCT
GGACTGAGAGTGGCTTTTCACAATGGAAGGGATCAGTAATTTCAAGACACCAAGCAAATTA
TCAGAAAAAAGAAATCTGTATTATGTTCAACTCCAACATAAAATATCCCGGCCTCTCCG
TTTATGCAGAAGCTTGGCTTTGGTACTGGGGTAAATGTGTACCTAATGAAAAGATCTCCA
AGAGGTTTGTCTCATTCTCCTTGGGCTGTAAAAAAGATTAATCCTATATGTAATGATCAT
TATCGAAGTGTGTATCAAAAGAGACTAATGGATGAAGCTAAGATTTTGAAAAGCCTTCAT
CATCCAAAACATTGTTGGTTATCGTGCTTTTACTGAAGCCAATGATGGCAGTCTGTGTCTT
GCTATGGAATATGGAGGTGAAAAGTCTCTAAATGACTTAATAGAAGAACGATATAAAGCC
AGCCAAGATCCTTTTCCAGCAGCCATAATTTTAAAGTTGCTTTGAATATGGCAAGAGGG
TTAAAGTATCTGCACCAAGAAAAGAACTGCTTCATGGAGACATAAAGTCTTCAAATGTT
GTAATTAAGGCGATTTTGAAACAAATAAAACTGTGTATGTAGGAGTCTCTTACCCTG
GATGAAAATATGACTGTGACTGACCCCTGAGGCTTGTTACATTGGCACAGAGCCATGGGAA
CCCAAAGAAGCTGTGGAGGAGAATGGTGTATTACTGACAAGGCAGACATATTTGCCTTT
GGCCTTACTTTGTGGGAAATGATGACTTTATCGATTCCACACATTAATCTTTCAAATGAT
GATGATGAAGATAAACTTTTGATGAAAGTGATTTTGATGATGAAGCATACTATGCA
GCGTTGGGAACCTAGGCCACCTATTAATATGGAAGAAGCTGGATGAATCATACCAGAAAGTA
ATTGAACTCTTCTGTATGCACTAATGAAGACCCTAAAGATCGTCCTTCTGCTGCACAC
ATTGTTGAAGCTCTGGAACAGATGTCTAGTGATCATCTCAGCTGAAGTGTGGCTTGCGT
AAATAACTGTTTATTCCAAAATATTTACATAGTTACTATCAGTAGTTATTAGACTCTAAA
ATTGGCATATTTGAGGACCATAGTTTCTTGTTAACATATGGATAACTATTTCTAATATGA
AATATGCTTATATTGGCTATAAGCACTTGGAAATGTACTGGGTTTTCTGTAAAGTTTTAG
AACTAGCTACATAAGTACTTTGATACTGCTCATGCTGACTTAAACACTAGCAGTAAAA
CGCTGTAAACTGTAACATTAAATTTGAATGACCATTACTTTTATTAATGATCTTTCTTAA
TATTCTATATTTAATGGATCTACTGACATTAGCACTTTGTACAGTACAAAATAAAGTCT
ACATTTGTTTTAAACACTGAACCTTTTGTGTATGTGTTTATCAAATGATACTGGAAGCT
GAGGAGAATATGCCTCAAAAAGAGTAGCTCCTTGGATACTTCAGACTCTGGTTACAGATT
GTCTTGATCTCTTGGATCTCCTCAGATCTTTGGTTTTTGCTTTAATTTATTAAATGTATT
TTCCATACTGAGTTTAAATTTTATTAATTTGTACCTTAAGCATTTCCAGCTGTGTAAAA
ACAATAAACTCAAATAGGATGATAAAGAATAAAGGACACTTTGGGTACCAGAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 38

MEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFMQKLGFGTG VNVYLMKRSPRGLSHSP
WAVKKINPICNDHYRSVYQKRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGGE
KSLNDLIEERYKASQDPFPAAIILKVALNMARGLKYLHQEKKLLHGDIKSSNVVIKGDFF
TIKICDVGVSPLDENMTVTDPEACYIGTEPWKPKEAVEENGVITDKADIFAFGLTLWEM
MTLSIPHINLSNDDDDKDTFDESDFDDEAYYAALGTRPPINMEELDESYQKVIELFSVC
TNEDPKDRPSAAHIVEALETDV

N-glycosylation site.

196-199
249-252

cAMP- and cGMP-dependent protein kinase phosphorylation site.

16-19

N-myristoylation site.

41-46
118-123

Serine/Threonine protein kinases active-site signature.

163-175

Protein kinase domain
32-320

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FIGURE 39

GTGCGATCCCGGGCCCGAGGGCATCAGACGGCGGCTGATTAGCTCCGGTTTGCATCACCC
GGACCGGGGGATTAGCTCCGGTTTGCATCACCCGGACCGGGGGCCGGGCGCGCACGAGAC
TCGCAGCGGAAGTGGAGGCGGCTCCGCGCGCGTCCGCTGCTAGGACCGGGCAGGGCTGG
AGCTGGGCTGGGATCCCGAGCTCGGCAGCAGCGCAGCGGGCCGGCCACCTGCTGGTGCC
CTGGAGGCTCTGAGCCCCGGCGGCGCCCGGGCCACGCGGAACGACGGGGCGAGATCGGA
GCCACCCCTCTAGCTGCTCCTGCGGGTTCCCTGTCCAGGAAGAAGCGGTTGGAGTTGGAT
GACAACTTAGATACCGAGCGTCCCGTCCAGAAACGAGCTCGAAGTGGGCCCCAGCCCAGA
CTGCCCCCTGCTGTGCCCCCTGAGCCCACCTACTGCTCCAGATCGTGCAACTGCTGTG
GCCACTGCCCTCCCGTCTTGGGCCCTATGTCTCCTTGGAGCCCCGAGGAGGGCGGGCGGGCC
TACCAGGECCTGCACTGCCCTACAGGCACTGAGTATACCTGCAAGGTGTACCCCGTCCAG
GAAGCCCCGGCCGTGCTGGAGCCCTATGCGCGGCTGCCCCCGCACAAAGCATGTGGCTCGG
CCCACTGAGGTCCTGGCTGGTACCCAGCTCCTCTACGCCTTTTTTCACTCGGACCCATGGG
GACATGCACAGCCTGGTGCGAAGCCGCCACCGTATCCCTGAGCCTGAGGCTGCCGTGCTC
TTCCGCCAGATGGCCACCGCCCTGGCGCACTGTACACAGCACGGTCTGGTCTGCGTGAT
CTCAAGCTGTGTGCTTTGTCTTCGCTGACCGTGAGAGGAAGAAGCTGGTGCTGGAGAAC
CTGGAGGACTCCTGCGTGCTGACTGGGCCAGATGATTCCCTGTGGGACAAGCACGCGTGC
CCAGCCTACGTGGGACCTGAGATACTCAGCTCACGGGCCTCATACTCGGGCAAGGCAGCC
GATGTCTGGAGCCTGGGCGTGGCGCTCTTACCATGCTGGCCGGCCACTACCCCTTCCAG
GACTCGGAGCCTGTCTGCTCTTTCGGCAAGATCCGCCGCGGGGCCTACGCCTTGCCTGCA
GGCCTCTCGGCCCCCTGCCCGCTGTCTGGTTTCGCTGCCTCCTTCGTGGGAGCCAGCTGAA
CGGCTCACAGCCACAGGCATCCTCCTGCACCCCTGGCTGCGACAGGACCCGATGCCCTTA
GCCCCAACCCGATCCCATCTCTGGGAGGCTGCCCAGGTGGTCCCTGATGGTCTGGGGCTG
GACGAAGCCAGGGAAGAGGAGGGAGACAGAGAAGTGGTTCTGTATGGCTAGGACCACCCT
ACTACACGCTCAGCTGCCAACAGTGGATTGAGTTTGGGGGTAGCTCCAAGCCTTCTCCTG
CCTCTGAAGTGAAGCAACCTTCACTGCCTTCCAGAAGGGAGAAAGGCAGAAGCCTGTGT
GGAGTGTGCTGTGTACACATCTGCTTTGTTCCACACACATGCAGTTCTCTGCTTGGGTGCT
TATCAGGTGCCAAGCCCTGTTCTCGGTGCTGGGAGTACAGCAGTGAGCAAAGGAGACAAT
ATTCCTGCTCACAGAGATGACAACTGGCATCCTTGAGCTGACAACTTTTCCATGAC
CATAGGTCACTGTCTACACTGGGTACACTTTGTACCAAGTGTGCGCCTCCACTGATGCTGG
TGCTCAGGCACCTCTGTCCAAGGACAATCCCTTTCACAAACAAACCAGCTGCCTTTGTAT
CTTGTACCTTTTTCAGAGAAAGGGAGGTATCCCTGTGCCAAAGGCTCCAGGCCTCTCCCT
GCAACTCAGGACCCAAGCCAGCTCACTCTGGGAAGTGTGTTCCCAGCATCTCTGTCTC
TTGATTAAGAGATTCTCCTTCCAGGCCTAAGCCTGGGATTTGGGCCAGAGATAAGAATCC
AAACTATGAGGCTAGTTCTTGTCTAACTCAAGACTGTTCTGGAATGAGGGTCCAGGCCTG
TCAACCATGGGGCTTCTGACCTGAGCACCAAGGTTGAGGGACAGGATTAGGCAGGGTCTG
TCCTGTGGCCACCTGGAAAGTCCAGGTGGGACTCTTCTGGGGACACTTGGGGTCCACAA
TCCCAGGTCCATACTCTAGGTTTTTGATACCATGAGTATGTATGTTTACCTGTGCCTAAT
AAAGGAGAATTATGAAATAAAAAAAAAAAAAAAAAA

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FIGURE 40

MRATPLAAPAGSLSRKKRLEDDNLDTERPVQKRARSGPQPRLPCLLPSPPTAPDRAT
AVATASRLGPYVLLPEEGGRAYQALHCPTGTEYTCKVYPVQEAPAVLEPYARLPPHKHV
ARPTEVLAGTQLLYAFFTRTHGDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVL
RDLKLCRFVFADRERKKLVLENLEDSVLTGPDDSLWDKHACPAYVGPEILSSRASYSK
AADVWSLGVALEFTMLAGHYPFQDSEPVLLFGKIRRGAYALPAGLSAPARCLVRCLLRREP
AERLTATGILLHPWLRQDPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLG

N-myristoylation site.

91-96
341-346

Protein kinase domain

71-315

45/46

FIGURE 41

GAAGTTTCTCACTAGGGTCTTCTCTGGCCCAGCCTTTGACTGAAGCTGGTCTGGAGACAG
GGGCATTAGAGAAGTGACTCATAGATGGCCTAAAGAAGCGGGGCCACTCAAGGACCCAGG
ACAGAGGGAAGAGGGCCAACCCAGCTGGACCACAGGCAAACCCATTGCCCTTTGAGAGAA
AGAAGAGGACCCGGTGAACATGCTGCTGCTGAAGAAACACACGGAGGACATCAGCAGCG
TCTACGAGATCCGCGAGAGGCTCGGCTCGGGTGCCTTCTCCGAGGTGGTGTGGCCCAGG
AGCGGGGCTCCGCACACCTCGTGGCCCTCAAGTGCATCCCCAAGAAGGCCCTCCGGGGCA
AGGAGGCCCTGGTGGAGAACGAGATCGCAGTGTCCGTAGGATCAGTCACCCCAACATCG
TCGCTCTGGAGGATGTCCACGAGAGCCCTTCCACCTCTACCTGGCCATGGAAGTGGTGA
CGGGTGGCGAGCTGTTTGACCGCATCATGGAGCGCGGCTCCTACACAGAGAAGGATGCCA
GCCATCTGGTGGGTGAGTCCCTTGGCGCCGTCTCCTACCTGCACAGCCTGGGGATCGTGC
ACCGGGACCTCAAGCCCGAAAACCTCCTGTATGCCACGCCCTTTGAGGACTCGAAGATCA
TGGTCTCTGACTTTGGACTCTCCAAAATCCAGGCTGGGAACATGCTAGGCACCGCCTGTG
GGACCCCTGGATATGTGGCCCCAGAGCTCTTGGAGCAGAAACCTACGGGAAGGCCGTAG
ATGTGTGGGCCCTGGGCGTCATCTCCTACATCCTGCTGTGTGGGTACCCCCCTTCTACG
ACGAGAGCGACCCTGAGCTCTCAGCCAGATCCTGAGGGCCAGCTATGAGTTTGACTXTC
CTTTCTGGGATGACATCTCAGAATCAGGCAAAGACTTTATTTCGGCACCTTCTGGAGCGAG
ACCTTCAGAAGAGGTTACCTGCCAACAGGCCCTTGCGGGACCTTTGGATCTTTTGGGACA
CAGGCTTTGGCAGGGACATCTTAGGGTTTGTCTAGTGAGCAGATCCGGAAGAACTTTGCTT
GGACACACTGGAAGCGAGCCTTCAATGCCACCTTGTTCCTGCGCCACATCCGGAAGCTGG
GGCAGATCCCAGAGGGCGAGGGGGCCTCTGAGCAGGGCATGGSCCGXCACAGCCACTXAG
GCCTTCGTGCTGGCCAGCCCCCAAGTGGTGATGCCCAGGXAGATGCCGAGGCCAAGTGG
AXTGAXCCCCAGATTTXCTTXC

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FIGURE 42

MLLLKKHTEDISSVYEIRERLGSGAFSEVVLAQERGS AHLVALKCIPKKALRGKEALVEN
EIAVLRRISHPNIVALEDVHESPSHLYLAMELVTGGELFDRIMERGSYTEKDASHLVGQV
LGAVSYLHSLGIVHRDLKPENLLYATPFEDSKIMVSDFGLSKIQAGNMLGTACGTPGYVA
PELLEQKPYGKAVDVWALGVISYILLCGYPPFFYDESDPELFSQILRASYEFDXPFWD
DIS ESGKDFIRHLLERDLQKRFTCQQALRDLWIFWDTGFGRDILGFVSEQIRKNFAWTHWKRA
FNATLFLRHIRKLGQIPEGEGASEQGMXRHSHXGLRAGQPPKW

N-glycosylation site.

302-305

cAMP- and cGMP-dependent protein kinase phosphorylation site.

5-8

66-69

257-260

Tyrosine kinase phosphorylation site.

101-108

N-myristoylation site.

118-123

166-171

170-175

334-339

Serine/Threonine protein kinases active-site signature.

132-144

Protein kinase domain

15-270